



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 175861

TO: Jeanine Goldberg
Location: rem/2D15/2C70
Art Unit: 1634
Tuesday, January 10, 2006
Case Serial Number: 09/954586

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1a69
Phone: 571-272-2518 *POB*

barbara.obryen@uspto.gov

Search Notes

RUSH

This Page Blank (uspto)

STIC-Biotech/ChemLib

175861

MEJ

From: Chan, Christina
Sent: Friday, January 06, 2006 1:23 PM
To: Goldberg, Jeanine; Fredman, Jeffrey; STIC-Biotech/ChemLib
Subject: RE: ALLOWANCE AF Search for 09/954586

Please ~~rush~~ Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644
(571)-272-0841
Remsen, 3E89

RECEIVED
JAN - 6 2006
STIC

-----Original Message-----

From: Goldberg, Jeanine
Sent: Friday, January 06, 2006 11:44 AM
To: Chan, Christina; Fredman, Jeffrey
Subject: ALLOWANCE AF Search for 09/954586

Please search SEQ ID NO: 46 and 59.

THANK YOU!
Jeanine

Jeanine Anne Goldberg
1634
571-272-0743
REM 2D15
Mailbox: 2C70

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model
Run on: January 9, 2006, 18:14:32 ; Search time 2255 Seconds
(without alignments)
579.778 Million cell updates/sec

Title: US-09-954-586-46
Perfect score: 23
Sequence: 1 ggataaccgtggaattcttagag 23

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues
Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba.*
2: gb_in.*
3: gb_env.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pr.*
9: gb_ro.*
10: gb_ats.*
11: gb_ey.*
12: gb_un.*
13: gb_vi.*
14: gb_htg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	23	100.0	23	6	AX421406	Sequence
C 3	23	100.0	23	6	AX421412	Sequence
C 4	23	100.0	23	6	AX421418	Sequence
5	23	100.0	32	6	AX421383	Sequence
6	23	100.0	32	6	AX421387	Sequence
C 7	23	100.0	32	6	AX421391	Sequence
C 8	23	100.0	32	6	AX421395	Sequence
9	23	100.0	143	3	AB046950	Endophyte
10	23	100.0	144	3	AB046947	Endophyte
11	23	100.0	144	3	AB046948	Endophyte
12	23	100.0	144	3	AB046949	Endophyte
13	23	100.0	145	15	GSU25153	Glomus sp.
14	23	100.0	145	15	SSU25155	Scutellospo
15	23	100.0	145	15	SSU25156	Scutellospo
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20	23	100.0	145	15	AF062706	Scutellospo
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22	23	100.0	146	15	AB046942	Glomus sp
23	23	100.0	146	15	AB046943	Glomus sp
24	23	100.0	146	15	AB046944	Glomus sp
25	23	100.0	146	15	AB046945	Glomus sp
26	23	100.0	146	15	GSU25154	Glomus sp.
27	23	100.0	146	15	AF062705	Scutellospo
28	23	100.0	152	15	AB046940	Acaulospor
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31	23	100.0	153	15	AB046941	Acaulospor
32	23	100.0	153	15	ASU25151	Acaulospor
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ALIGNMENTS

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DEFINITION Sequence 46 from Patent WO0222890.
ACCESSION AX421400
VERSION AX421400.1 GI:21524795
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1
AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE Compositions, methods and kits for determining the presence of
JOURNAL Cryptosporidium organisms in a test sample
Patent: WO 0222890-A 46 21-MAR-2002;
FEATURES Gen-Probe Incorporated (US)
source Location/Qualifiers
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LOCUS AX421406 23 bp RNA linear PAT 18-JUN-2002						
DEFINITION Sequence 52 from Patent WO0222890.						
ACCESSION AX421406						
VERSION AX421406.1 GI:21524801						
KEYWORDS synthetic construct						
SOURCE synthetic construct						
ORGANISM						

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other sequences; artificial sequences.
1 Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
Compositions, methods and kits for determining the presence of
cryptosporidium organisms in a test sample
Patent: WO 0222890-A 52 21-MAR-2002;
Gen-Probe Incorporated (US)
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LOCUS AX421412 23 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 58 from Patent WO0222890.
ACCESSION AX421412
VERSION AX421412.1 GI:21524807
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
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REFERENCE
AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE Compositions, methods and kits for determining the presence of
cryptosporidium organisms in a test sample
JOURNAL Patent: WO 0222890-A 58 21-MAR-2002;
Gen-Probe Incorporated (US)
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DEFINITION Sequence 64 from Patent WO0222890.
ACCESSION AX421418
VERSION AX421418.1 GI:21524813
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
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REFERENCE
AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE Compositions, methods and kits for determining the presence of
cryptosporidium organisms in a test sample
JOURNAL Patent: WO 0222890-A 64 21-MAR-2002;
Gen-Probe Incorporated (US)
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DEFINITION Sequence 29 from Patent WO0222890.
ACCESSION AX421383
VERSION AX421383.1 GI:21524778
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
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REFERENCE
AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE Compositions, methods and kits for determining the presence of
cryptosporidium organisms in a test sample
JOURNAL Patent: WO 0222890-A 29 21-MAR-2002;
Gen-Probe Incorporated (US)
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DEFINITION Sequence 33 from Patent WO0222890.
ACCESSION AX421387
VERSION AX421387.1 GI:21524782
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
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REFERENCE
AUTHORS Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE Compositions, methods and kits for determining the presence of
cryptosporidium organisms in a test sample
JOURNAL Patent: WO 0222890-A 33 21-MAR-2002;
Gen-Probe Incorporated (US)
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ACCESSION AB046950
VERSION AB046950.1 GI:10039400
KEYWORDS ENV.
SOURCE endophyte DG vagiga5
ORGANISM endophyte DG vagiga5
          Eukaryota; Fungi; Ascomycota; environmental samples.

REFERENCE
AUTHORS Saito,K., Nishiwaki,A. and Sugawara,K.
TITLE Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRNA
JOURNAL Grassl. Sci. 47, 1-8 (2001)
AUTHORS Saito,K.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2000) Katsuharu Saito, National Institute of
          Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno,
          Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp,
          Tel:81-287-37-7691, Fax:81-287-36-6629)

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RESULT 10
AB046947
LOCUS 144 bp DNA linear ENV 27-JUL-2005
DEFINITION Endophyte DG vagiga2 gene for small subunit ribosomal RNA.
ACCESSION AB046947
VERSION AB046947.1 GI:10039397
KEYWORDS ENV.
SOURCE endophyte DG vagiga2
          Eukaryota; Fungi; Ascomycota; environmental samples.

REFERENCE
AUTHORS Saito,K., Nishiwaki,A. and Sugawara,K.
TITLE Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRNA
JOURNAL Grassl. Sci. 47, 1-8 (2001)
AUTHORS Saito,K.
TITLE Direct Submission
JOURNAL Submitted (04-AUG-2000) Katsuharu Saito, National Institute of
          Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno,
          Tochigi, 329-2793, Japan (E-mail:saitok@affrc.go.jp,
          Tel:81-287-37-7691, Fax:81-287-36-6629)

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LOCUS      144 bp      DNA      linear      ENV 27-JUL-2005
DEFINITION Endophyte DG vagiga3 gene for small subunit ribosomal RNA.
ACCESSION  AB046948
VERSION     AB046948.1 GI:10039398
KEYWORDS    endophyte DG vagiga3
SOURCE      Eukaryota; Fungi; Ascomycota; environmental samples.
ORGANISM
REFERENCE 1 Saito, K., Nishiwaki, A. and Sugawara, K.
AUTHORS    Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRNA
TITLE      Genes from field-collected roots
JOURNAL    Grassl. Sci. 47, 1-8 (2001)
REFERENCE 2 (bases 1 to 144)
AUTHORS    Saito, K.
TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2000) Katsuharu Saito, National Institute of
           Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno,
           Tochigi, 329-2793, Japan (E-mail: saito@affrc.go.jp,
           Tel: 81-287-37-7691, Fax: 81-287-36-6629)
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LOCUS      144 bp      DNA      linear      ENV 27-JUL-2005
DEFINITION Endophyte DG vagiga4 gene for small subunit ribosomal RNA.
ACCESSION  AB046949
VERSION     AB046949.1 GI:10039399
KEYWORDS    endophyte DG vagiga4
SOURCE      Eukaryota; Fungi; Ascomycota; environmental samples.
ORGANISM
REFERENCE 1 Saito, K., Nishiwaki, A. and Sugawara, K.
AUTHORS    Nested PCR amplification of arbuscular mycorrhizal fungal 18S rRNA
TITLE      Genes from field-collected roots
JOURNAL    Grassl. Sci. 47, 1-8 (2001)
REFERENCE 2 (bases 1 to 144)
AUTHORS    Saito, K.
TITLE      Direct Submission
JOURNAL    Submitted (04-AUG-2000) Katsuharu Saito, National Institute of
           Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno,
           Tochigi, 329-2793, Japan (E-mail: saito@affrc.go.jp,
           Tel: 81-287-37-7691, Fax: 81-287-36-6629)
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DEFINITION Glomus sp. Glol 18S ribosomal RNA gene, partial sequence.
ACCESSION  U25153
VERSION     U25153.1 GI:806866
KEYWORDS    Glomus sp. Glol
SOURCE      Glomus sp. Glol
ORGANISM    Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;
           Glomeraceae; Glomus.
REFERENCE 1 (bases 1 to 145)
AUTHORS    Clapp, J. P., Young, J. W., Merryweather, J. W. and Fitter, A. H.
TITLE      Diversity of fungal symbionts in arbuscular mycorrhizas from a
           natural community
JOURNAL    New Phytol. 130 (2), 259-265 (1995)
REFERENCE 2 (bases 1 to 145)
AUTHORS    Clapp, J. P.
TITLE      Direct Submission
JOURNAL    Submitted (18-APR-1995) Justin P. Clapp, Biology, University of
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RESULT 14
SSU25155

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JOURNAL    Submitted (04-AUG-2000) Katsuharu Saito, National Institute of
           Livestock and Grassland Science; 768 Senbonmatsu, Nishinasuno,
           Tochigi, 329-2793, Japan (E-mail: saito@affrc.go.jp,
           Tel: 81-287-37-7691, Fax: 81-287-36-6629)
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DEFINITION Glomus sp. Glol 18S ribosomal RNA gene, partial sequence.
ACCESSION  U25153
VERSION     U25153.1 GI:806866
KEYWORDS    Glomus sp. Glol
SOURCE      Glomus sp. Glol
ORGANISM    Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;
           Glomeraceae; Glomus.
REFERENCE 1 (bases 1 to 145)
AUTHORS    Clapp, J. P., Young, J. W., Merryweather, J. W. and Fitter, A. H.
TITLE      Diversity of fungal symbionts in arbuscular mycorrhizas from a
           natural community
JOURNAL    New Phytol. 130 (2), 259-265 (1995)
REFERENCE 2 (bases 1 to 145)
AUTHORS    Clapp, J. P.
TITLE      Direct Submission
JOURNAL    Submitted (18-APR-1995) Justin P. Clapp, Biology, University of
           York, Heslington, York, North Yorkshire YO1 5YW, England
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RESULT 14
SSU25155

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ACCESSION U25155
VERSION U25155.1 GI:806868
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SOURCE
ORGANISM Scutellospora sp. Scut2
Scutellospora sp. Scut2
Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Diversisporales;
Gigasporaceae; Scutellospora.
REFERENCE 1 (bases 1 to 145)
AUTHORS Clapp,J.P., Young,J.W., Merryweather,J.W. and Fitter,A.H.
TITLE Diversity of fungal symbionts in arbuscular mycorrhizas from a
natural community
JOURNAL New Phytol. 130 (2), 259-265 (1995)
REFERENCE 2 (bases 1 to 145)
AUTHORS Clapp,J.P.
TITLE Direct Submission
JOURNAL Submitted (18-APR-1995) Justin P. Clapp, Biology, University of
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SSU25156 145 bp DNA linear PLN 22-JAN-2003
LOCUS Scutellospora sp. scut1 18S ribosomal RNA gene, partial sequence.
ACCESSION U25156
VERSION U25156.1 GI:806869
KEYWORDS
SOURCE
ORGANISM Scutellospora sp. Scut1
Scutellospora sp. Scut1
Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Diversisporales;
Gigasporaceae; Scutellospora.
REFERENCE 1 (bases 1 to 145)
AUTHORS Clapp,J.P., Young,J.W., Merryweather,J.W. and Fitter,A.H.
TITLE Diversity of fungal symbionts in arbuscular mycorrhizas from a
natural community
JOURNAL New Phytol. 130 (2), 259-265 (1995)
REFERENCE 2 (bases 1 to 145)
AUTHORS Clapp,J.P.
TITLE Direct Submission
JOURNAL Submitted (18-APR-1995) Justin P. Clapp, Biology, University of
York, Heslington, York, North Yorkshire YO1 5YW, England
FEATURES
source
1..145
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/mol_type="genomic DNA"
/specific_host="Hyacinthoides non-scripta"
/db_xref="taxon:108482"
/clone="scut1"
/tissue_type="intraradical hyphae"
<1..>145
rRNA

/product="18S ribosomal RNA"
/note="corresponds to bases 83-277 of the 18S ribosomal
RNA gene of Saccharomyces cerevisiae, GenBank Accession
Number J01353"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 61 GGATAACCGTGGTAATTCCTAGAG 83
Search completed: January 9, 2006, 19:54:13
Job time : 2260 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 16:34:41 ; Search time 327 Seconds
(without alignments)

468.770 Million cell updates/sec

Title: US-09-954-586-46

Perfect score: 23

Sequence: 1 ggataaccgtggtaattcttagag 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq_21.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1980s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2002bs.*
- 8: Geneseqn2003as.*
- 9: Geneseqn2003bs.*
- 10: Geneseqn2003cs.*
- 11: Geneseqn2003ds.*
- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*
- 14: Geneseqn2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	23	AAD38426	Aad38426 Cryptospor
C 2	23	100.0	23	AAD38438	Aad38438 Cryptospor
C 3	23	100.0	23	AAD38444	Aad38444 Cryptospor
4	23	100.0	23	AAD38432	Aad38432 Cryptospor
5	23	100.0	32	AAD38409	Aad38409 Cryptospor
C 6	23	100.0	32	AAD38421	Aad38421 Cryptospor
7	23	100.0	32	AAD38413	Aad38413 Cryptospor
C 8	23	100.0	32	AAD38417	Aad38417 Cryptospor
C 9	23	100.0	384	ADY98693	Ady98693 T_reesei
10	23	100.0	444	AAQ71869	Aaq71869 G. margar
11	23	100.0	447	AAQ71867	Aaq71867 G. vesicu
12	23	100.0	447	AAQ71870	Aaq71870 E. pisifo
13	23	100.0	447	AAQ71868	Aaq71868 G. intrax
14	23	100.0	488	ADR99351	Adr99351 Acremoniu
15	23	100.0	501	ABS53676	Ab553676 Filamento
16	23	100.0	538	ADY98694	Ady98694 T_reesei
17	23	100.0	540	ADY98695	Ady98695 T_reesei
C 18	23	100.0	570	AAF08498	Aaf08498 Fusarium
C 19	23	100.0	570	ADU52539	Adu52539 Fusarium

C	20	23	100.0	570	14	AD290542	Ad290542 Fusarium
	21	23	100.0	617	3	AAF10913	Aaf10913 Fusarium
	22	23	100.0	617	13	ADU54954	Adu54954 Fusarium
	23	23	100.0	617	14	AD292957	Ad292957 Fusarium
	24	23	100.0	1328	10	AB280030	Ab280030 Xylariale
	25	23	100.0	1247	10	ACA61067	Aca61067 Phyllosti
	26	23	100.0	1727	6	ABV78726	C. sinens
	27	23	100.0	1731	4	AAI68286	Bulgaria
	28	23	100.0	1731	6	ABA01154	Deuteromy
	29	23	100.0	1731	13	ADP79725	Anti-tumo
	30	23	100.0	1732	12	ADH43081	18s rRNA
	31	23	100.0	1733	13	ADP79724	Anti-tumo
	32	23	100.0	1743	11	ADZ11854	Geotrichu
	33	23	100.0	1745	6	ABA01152	Deuteromy
	34	23	100.0	1750	2	AAT90818	C. parvum
	35	23	100.0	1750	3	AAA46368	Nucleotid
	36	23	100.0	1761	6	ABV78699	C. crassi
	37	23	100.0	1766	6	ABV78720	C. sinens
	38	23	100.0	1766	6	ABV78708	C. sinens
	39	23	100.0	1766	6	ABV78714	C. sinens
	40	23	100.0	1766	6	ABV78711	C. sinens
	41	23	100.0	1766	6	ABV78717	C. sinens
	42	23	100.0	1766	6	ABV78705	C. sinens
	43	23	100.0	1766	6	ABV78702	C. sinens
	44	23	100.0	1766	6	ABV78723	C. sinens
	45	23	100.0	1771	2	AAV61668	Fusarium

ALIGNMENTS

RESULT 1

AAD38426
ID AAD38426 standard; DNA; 23 BP.
XX
AC AAD38426;
XX
DT 10-SEP-2002 (first entry)
XX
DE Cryptosporidium sp. target DNA #8.
XX
KW Hybridisation; amplification; detection; da.
XX
OS Cryptosporidium sp.
XX
PN WO200222890-A2.
XX
PD 21-MAR-2002.
XX
PF 11-SEP-2001; 2001WO-US042192.
XX
PR 12-SEP-2000; 2000US-0232028P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Cunningham MM, Stull PD, Weisburg WG;
XX
DR WPI; 2002-454395/48.
XX
PT Novel oligonucleotides functioning as hybridization probes, helper probes and/or primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms, useful for detecting the organism in a test sample.
XX
PS Claim 23; Page 8; 133pp; English.
XX
CC The invention relates to oligonucleotides functioning as hybridisation assay probes, helper probes and/or amplification primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms. Probes and primers of the invention are useful for detecting the presence of Cryptosporidium organisms in general and C. parvum organisms in particular in a test sample. The present sequence is Cryptosporidium sp. target DNA

DR WPI; 2002-454395/48.
XX Novel oligonucleotides functioning as hybridization probes, helper probes
PT and/or primers, targeted to nucleic acid sequences derived from
PT Cryptosporidium organisms, useful for detecting the organism in a test
PT sample.
XX
XX
XX Claim 23; Page 8; 133pp; English.
XX
CC The invention relates to oligonucleotides functioning as hybridisation
CC assay probes, helper probes and/or amplification primers, targeted to
CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and
CC primers of the invention are useful for detecting the presence of
CC Cryptosporidium organisms in general and C. parvum organisms in
CC particular in a test sample. The present sequence is Cryptosporidium sp.
CC target RNA
XX
SQ Sequence 23 BP; 7 A; 3 C; 7 G; 0 T; 6 U; 0 Other;

Query Match 100.0%; Score 23; DB 6; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.18; Mismatches 0; Indels 0; Gaps 0;
Matches 17; Conservative 6;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23
|||:||||:||||:||||:||||:
DB 1 GGAUACCGUGUAUUCUAGAG 23

RESULT 5
AAD38409
ID AAD38409 standard; DNA; 32 BP.
XX
AC AAD38409;
XX
DT 10-SEP-2002 (first entry)
XX
DE Cryptosporidium parvum target DNA #9.
XX
KW Hybridisation; amplification; detection; ds.
XX
OS Cryptosporidium parvum.
XX
EN WO200222890-A2.
XX
PD 21-MAR-2002.
XX
PF 11-SEP-2001; 2001WO-US042192.
XX
PR 12-SEP-2000; 2000US-0232028P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Cunningham MM, Stull PD, Weisburg WG;
XX
DR WPI; 2002-454395/48.

Novel oligonucleotides functioning as hybridization probes, helper probes
and/or primers, targeted to nucleic acid sequences derived from
PT Cryptosporidium organisms, useful for detecting the organism in a test
PT sample.
XX
XX Claim 102; Page 6; 133pp; English.
XX
CC The invention relates to oligonucleotides functioning as hybridisation
CC assay probes, helper probes and/or amplification primers, targeted to
CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and
CC primers of the invention are useful for detecting the presence of
CC Cryptosporidium organisms in general and C. parvum organisms in
CC particular in a test sample. The present sequence is C. parvum target DNA
XX
SQ Sequence 32 BP; 11 A; 5 C; 7 G; 9 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 6; Length 32;

Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGATAACCGTGGTAATTTCTAGAG 23
|||:||||:||||:||||:||||:
DB 1 GGAUACCGUGTAATTTCTAGAG 23

RESULT 6
AAD38421/C
ID AAD38421 standard; RNA; 32 BP.
XX
AC AAD38421;
XX
DT 10-SEP-2002 (first entry)
XX
DE Cryptosporidium parvum target RNA #13.
XX
KW Hybridisation; amplification; detection; ss.
XX
OS Cryptosporidium parvum.
XX
EN WO200222890-A2.
XX
PD 21-MAR-2002.
XX
PF 11-SEP-2001; 2001WO-US042192.
XX
PR 12-SEP-2000; 2000US-0232028P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Cunningham MM, Stull PD, Weisburg WG;
XX
DR WPI; 2002-454395/48.

Novel oligonucleotides functioning as hybridization probes, helper probes
and/or primers, targeted to nucleic acid sequences derived from
PT Cryptosporidium organisms, useful for detecting the organism in a test
PT sample.
XX
XX Claim 102; Page 6; 133pp; English.
XX
CC The invention relates to oligonucleotides functioning as hybridisation
CC assay probes, helper probes and/or amplification primers, targeted to
CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and
CC primers of the invention are useful for detecting the presence of
CC Cryptosporidium organisms in general and C. parvum organisms in
CC particular in a test sample. The present sequence is C. parvum target RNA
XX
SQ Sequence 32 BP; 9 A; 7 C; 5 G; 0 T; 11 U; 0 Other;

Query Match 100.0%; Score 23; DB 6; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.19; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23
|||:||||:||||:||||:||||:
DB 32 GGAUACCGUGTAATTTCTAGAG 10

RESULT 7
AAD38413
ID AAD38413 standard; RNA; 32 BP.
XX
AC AAD38413;
XX
DT 10-SEP-2002 (first entry)
XX
DE Cryptosporidium parvum target RNA #9.
XX
KW Hybridisation; amplification; detection; ss.
XX

OS Cryptosporidium parvum.
 PN WO200222890-A2.
 XX 21-MAR-2002.
 PD 11-SEP-2001; 2001WO-US042192.
 PF 12-SEP-2000; 2000US-0232028P.
 PR (GENP-) GEN-PROBE INC.
 XX Cunningham MM, Stull PD, Weisburg WG;
 XX WPI; 2002-454395/48.
 DR Novel oligonucleotides functioning as hybridization probes, helper probes
 PT and/or primers, targeted to nucleic acid sequences derived from
 PT Cryptosporidium organisms, useful for detecting the organism in a test
 PT sample.
 XX
 PS Claim 102; Page 6; 133pp; English.
 XX The invention relates to oligonucleotides functioning as hybridisation
 CC assay probes, helper probes and/or amplification primers, targetted to
 CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and
 CC primers of the invention are useful for detecting the presence of
 CC Cryptosporidium organisms in general and C. parvum organisms in
 CC particular in a test sample. The present sequence is C. parvum target RNA
 CC
 XX Sequence 32 BP; 11 A; 5 C; 7 G; 0 T; 9 U; 0 Other;
 SQ
 Query Match 100.0%; Score 23; DB 6; Length 32;
 Best Local Similarity 73.9%; Pred. No. 0.19;
 Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGATACCGTGGTAAATTCCTAGAG 23
 Db 1 GGAUAACCGGUAUUCUAGAG 23
 RESULT 8
 AAD38417/c
 ID AAD38417 standard; DNA; 32 BP.
 XX
 AC AAD38417;
 XX
 DT 10-SEP-2002 (first entry)
 XX
 DE Cryptosporidium parvum target DNA #13.
 XX
 KW Hybridisation; amplification; detection; ds.
 XX
 OS Cryptosporidium parvum.
 XX
 PN WO200222890-A2.
 XX 21-MAR-2002.
 XX 11-SEP-2001; 2001WO-US042192.
 XX 12-SEP-2000; 2000US-0232028P.
 XX (GENP-) GEN-PROBE INC.
 XX Cunningham MM, Stull PD, Weisburg WG;
 XX WPI; 2002-454395/48.
 XX Novel oligonucleotides functioning as hybridization probes, helper probes
 PT and/or primers, targeted to nucleic acid sequences derived from
 PT Cryptosporidium organisms, useful for detecting the organism in a test
 PT sample.

XX Claim 102; Page 6; 133pp; English.
 PS The invention relates to oligonucleotides functioning as hybridisation
 CC assay probes, helper probes and/or amplification primers, targetted to
 CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and
 CC primers of the invention are useful for detecting the presence of
 CC Cryptosporidium organisms in general and C. parvum organisms in
 CC particular in a test sample. The present sequence is C. parvum target DNA
 CC
 XX Sequence 32 BP; 9 A; 7 C; 5 G; 11 T; 0 U; 0 Other;
 SQ
 Query Match 100.0%; Score 23; DB 6; Length 32;
 Best Local Similarity 100.0%; Pred. No. 0.19;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGATACCGTGGTAAATTCCTAGAG 23
 Db 32 GGATACCGTGGTAAATTCCTAGAG 10
 RESULT 9
 ADY98693/c
 ID ADY98693 standard; cDNA; 384 BP.
 XX
 AC ADY98693;
 XX
 DT 16-JUN-2005 (first entry)
 XX
 DE T_reesei suppressive subtractive hybridization (SSH) cDNA clone Seq 47.
 XX
 KW gene expression; suppressive subtractive hybridization; microarray;
 KW microorganism; ss.
 XX
 OS Hypocrea jecorina.
 XX
 PN US2005069934-A1.
 XX 31-MAR-2005.
 PD 24-SEP-2004; 2004US-00950009.
 PF 25-SEP-2003; 2003US-0506140P.
 PR (NOVO) NOVOZYMES BIOTECH INC.
 XX
 PA Berka R, Bashkistrova E, Rey M;
 XX WPI; 2005-271963/28.
 DR
 XX
 DE Monitoring differential expression of genes of two filamentous fungal
 PT cells, for e.g. discovering new genes, comprises adding labeled nucleic
 PT acids to an array of Trichoderma reesei expressed sequenced tags and
 PT detecting spots.
 XX
 PS Claim 1; SEQ ID NO 47; 27pp; English.
 XX
 CC This invention relates to a novel method for monitoring differential
 CC expression of genes in a filamentous fungal cell. Specifically, it refers
 CC to identifying differential gene expression occurring between two related
 CC filamentous fungal cells and comprises adding detection reporter labeled
 CC nucleic acids of filamentous fungal cells to a substrate array of
 CC Trichoderma reesei (T. reesei) expressed sequenced tags (ESTs), or
 CC suppression subtractive hybridization (SSH) clones and detecting a signal
 CC in the array. The present invention further describes a computer readable
 CC medium having for monitoring differential expression of several genes in
 CC a first filamentous fungal cell relative to expression of the same genes
 CC in one or more second filamentous fungal cells. It also provides a search
 CC unit for comparing a target sequence to a T. reesei EST sequence of the
 CC data storage unit to identify homologous sequences, and a retrieval unit
 CC for obtaining the homologous sequence(s). Accordingly, it provides a
 CC method useful for identifying microbial genes induced when the
 CC microorganism is grown on cellulose or corn stover, as well as for

CC discovering new genes, identifying possible functions of unknown open
 CC reading frames and monitoring gene copy number variation and stability.
 CC Note that this method utilizes an array where one spot equals one gene or
 CC open reading frame, which makes extensive follow-up characterization
 CC unnecessary since sequence information is available and EST and/or SSH
 CC microarrays can be organized based on function of the gene products. This
 CC polynucleotide sequence is a T. reesei SSH cDNA clone that forms part of
 CC the substrate array of the invention. NOTE: The SeqIDs 1-1188 referring
 CC to T. reesei ESTs or SSH clones or their combinations are available in
 CC electronic form from the USPTO web site
 CC (<http://seqdata.uspto.gov/sequence.html>; Document ID:20050069934).
 CC
 SQ Sequence 384 BP; 108 A; 83 C; 88 G; 105 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 14; Length 384;
 Best Local Similarity 100.0%; Pred. No. 0.23; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0;

Qy 1 GGATAACCGTGGTAATTTCTAGAG 23
 |||||
 Db 234 GGATAACCGTGGTAATTTCTAGAG 212

RESULT 10
 AAQ71869
 ID AAQ71869 standard; DNA; 444 BP.

XX AC AAQ71869;

XX DT 23-MAR-1995 (first entry)

XX DE G. margarita small ribosomal subunit RNA.

XX KW Nuclear 18S ribosomal gene; SSU; probe; primer;
 XX arbuscular endomycorrhizal fungi; plant; root; ds.

XX OS Gigaspora margarita.

XX XX CA2086136-A.

XX PD 24-JUN-1994.

XX PF 23-DEC-1992; 92CA-02086136.

XX PR 23-DEC-1992; 92CA-02086136.

XX PA (SIMO/) SIMON L.

XX PI Simon L, Lalonde M;

XX DR WPI; 1994-264577/33.

XX New oligonucleotide probes - used for the detection of arbuscular
 PT endomycorrhizal fungi in plant root samples.

XX PS Disclosure; Page 19; 40pp; English.

XX The gene sequence of the small ribosomal subunit RNA of arbuscular
 CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
 CC intraradices and Gigaspora margarita were compared with that of a non-
 CC arbuscular endomycorrhizal fungus, Endogone pisiformis, in order to
 CC design taxon specific primers/probes

XX SQ Sequence 444 BP; 134 A; 81 C; 104 G; 125 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 2; Length 444;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTTCTAGAG 23
 |||||
 Db 33 GGATAACCGTGGTAATTTCTAGAG 55

RESULT 11
 AAQ71867
 ID AAQ71867 standard; DNA; 447 BP.
 XX AC AAQ71867;
 XX DT 23-MAR-1995 (first entry)
 XX DE G. vesiculiferum small ribosomal subunit RNA.
 XX KW Nuclear 18S ribosomal gene; SSU; probe; primer;
 XX arbuscular endomycorrhizal fungi; plant; root; ds.

XX OS Glomus vesiculiferum.

XX PN CA2086136-A.

XX PD 24-JUN-1994.

XX PF 23-DEC-1992; 92CA-02086136.

XX PR 23-DEC-1992; 92CA-02086136.

XX PA (SIMO/) SIMON L.

XX PI Simon L, Lalonde M;

XX XX WPI; 1994-264577/33.

XX New oligonucleotide probes - used for the detection of arbuscular
 PT endomycorrhizal fungi in plant root samples.

XX PS Disclosure; Page 18; 40pp; English.

XX The gene sequence of the small ribosomal subunit RNA of arbuscular
 CC endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
 CC intraradices and Gigaspora margarita were compared with that of a non-
 CC arbuscular endomycorrhizal fungus, Endogone pisiformis, in order to
 CC design taxon specific primers/probes

XX SQ Sequence 447 BP; 135 A; 86 C; 107 G; 118 T; 0 U; 1 Other;

Query Match 100.0%; Score 23; DB 2; Length 447;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTTCTAGAG 23
 |||||
 Db 32 GGATAACCGTGGTAATTTCTAGAG 54

RESULT 12
 AAQ71870
 ID AAQ71870 standard; DNA; 447 BP.

XX AC AAQ71870;

XX DT 23-MAR-1995 (first entry)

XX DE E. pisiformis small ribosomal subunit RNA.

XX KW Nuclear 18S ribosomal gene; SSU; probe; primer;
 KW arbuscular endomycorrhizal fungi; plant; root; ds.

XX OS Endogone pisiformis.

XX FH Key Location/Qualifiers

FT misc_difference 116..135

FT /*tag= a

XX /note= "bases not determined"

XX PN CA2086136-A.

XX 24-JUN-1994.
 XX 23-DEC-1992; 92CA-02086136.
 XX 23-DEC-1992; 92CA-02086136.
 XX (SIMO/) SIMON L.
 XX Simon L, Lalonde M;
 XX WPI; 1994-264577/33.
 XX New oligonucleotide probes - used for the detection of arbuscular
 PT endomycorrhizal fungi in plant root samples.
 XX
 XX Disclosure; Page 20; 40pp; English.
 XX The gene sequence of the small ribosomal subunit RNA of arbuscular
 CC endomycorrhizal fungi obtained from *Glomus vesiculiferum*, *Glomus*
 CC intraradices and *Gigaspora margarita* were compared with that of a non-
 CC arbuscular endomycorrhizal fungus, *Endogone pisiformis*, in order to
 CC design taxon specific primers/probes
 XX
 XX Sequence 447 BP; 133 A; 77 C; 100 G; 117 T; 0 U; 20 Other;
 SQ
 Query Match 100.0%; Score 23; DB 2; Length 447;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGATAACCGTGGTAATTCCTAGAG 23
 Db 33 GGATAACCGTGGTAATTCCTAGAG 55
 RESULT 13
 ID AAQ71868 standard; DNA; 447 BP.
 XX
 AC AAQ71868;
 XX
 DT 23-MAR-1995 (first entry)
 XX
 XX G. intraradices small ribosomal subunit RNA.
 XX
 XX Nuclear 18S ribosomal gene; SSU; probe; primer;
 KW arbuscular endomycorrhizal fungi; plant; root; ds.
 XX
 XX *Glomus intraradices*.
 XX
 XX CA2086136-A.
 XX
 XX 24-JUN-1994.
 XX
 XX 23-DEC-1992; 92CA-02086136.
 XX
 XX 23-DEC-1992; 92CA-02086136.
 XX
 XX (SIMO/) SIMON L.
 XX
 XX Simon L, Lalonde M;
 XX WPI; 1994-264577/33.
 XX
 XX New oligonucleotide probes - used for the detection of arbuscular
 PT endomycorrhizal fungi in plant root samples.
 XX
 XX Disclosure; Page 19; 40pp; English.
 XX
 XX The gene sequence of the small ribosomal subunit RNA of arbuscular
 CC endomycorrhizal fungi obtained from *Glomus vesiculiferum*, *Glomus*
 CC intraradices and *Gigaspora margarita* were compared with that of a non-
 CC arbuscular endomycorrhizal fungus, *Endogone pisiformis*, in order to

CC design taxon specific primers/probes
 XX
 SQ Sequence 447 BP; 137 A; 86 C; 107 G; 117 T; 0 U; 0 Other;
 Query Match 100.0%; Score 23; DB 2; Length 447;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGATAACCGTGGTAATTCCTAGAG 23
 Db 32 GGATAACCGTGGTAATTCCTAGAG 54
 RESULT 14
 ID ADR99351 standard; DNA; 488 BP.
 XX
 AC ADR99351;
 XX
 DT 16-DEC-2004 (first entry)
 XX
 XX Acremonium 18S rDNA gene sequence.
 DE
 XX algicide; red tide; dinoflagellate; 18S rDNA gene; ds.
 KW
 XX
 XX Acremonium sp.
 XX
 XX JP2004262879-A.
 PN
 XX 24-SEP-2004.
 PD
 XX
 XX 04-MAR-2003; 2003JP-00056623.
 PF
 XX
 XX 04-MAR-2003; 2003JP-00056623.
 PR
 XX
 XX (KAIY-) KAIYO BIOTECHNOLOGY KENKYUSHO KK.
 PA
 XX
 XX WPI; 2004-672306/66.
 DR
 XX
 PT Novel cyclic peptide, useful as algicide for exterminating red tide
 PT containing dinoflagellates in seas, lakes, marshes, seashores, artificial
 PT ponds and pools.
 PT
 XX
 PS Disclosure; SEQ ID NO 1; 18pp; Japanese.
 XX
 XX The invention comprises a cyclic peptide which has algicide activity
 CC against red tide containing dinoflagellates, without exerting any
 CC influence on the environment. The cyclic peptide of the invention is
 CC useful as an algicide for exterminating red tide containing
 CC dinoflagellates belonging to *Prorocentrum*, *Heterocapsa* and *Gymnodinium*
 CC sp. in seas, lakes, marshes, seashores, artificial ponds and pools. The
 CC present DNA sequence represents an Acremonium 18S rDNA gene sequence that
 CC was used in the exemplification of the invention.
 XX
 SQ Sequence 488 BP; 138 A; 100 C; 117 G; 133 T; 0 U; 0 Other;
 Query Match 100.0%; Score 23; DB 13; Length 488;
 Best Local Similarity 100.0%; Pred. No. 0.23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGATAACCGTGGTAATTCCTAGAG 23
 Db 71 GGATAACCGTGGTAATTCCTAGAG 93
 RESULT 15
 ID ABS53676 standard; DNA; 501 BP.
 XX
 AC ABS53676;
 XX
 DT 20-NOV-2002 (first entry)
 XX

DE Filamentous fungi 18S rDNA partial sequence.
XX
XX Antimicrobial agent; slime; PCR; primer; ss; papermaking industry;
KW 18S rDNA; filamentous fungi.
XX
XX Ascomycota.
XX
XX WO200254865-A1.
XX
XX 18-JUL-2002.
XX
XX 08-JAN-2002; 2002WO-JP000012.
XX
XX 09-JAN-2001; 2001JP-00001427.
XX
XX 10-JUL-2001; 2001JP-00209845.
XX
XX 29-NOV-2001; 2001JP-00365004.
XX
XX (KURK) KURITA WATER IND LTD.
XX
XX Iizumi T, Suzuki H, Tashiro H;
XX
XX WPI; 2002-682647/73.
XX
XX New method, useful in screening anti-microbial agents for controlling
PT slimes in papermaking industry or monitoring anti-microbial effect,
PT comprises microbial analysis step and anti-microbial selection step.
XX
XX Example 10; Page 91-92; 94pp; Japanese.
XX
XX The invention relates to a method for selecting an anti-microbial agent,
CC comprising: (A) the microbial analysis step of analysing the microbial
CC phase of a sample based on DNA base sequences (e.g. by PCR); and (B) the
CC anti-microbial selection step by searching a database for matching and
CC extracting an industrial anti-microbial agent with optimum anti-microbial
CC properties. The method may be used to choose anti-microbial agents for
CC treatment of microorganism-containing samples, to monitor the effect of
CC added antimicrobial agent over time in a sample or process, to inhibit or
CC regulate slime in paper manufacturing and for the analysis of adherent on
CC paper products during manufacture, in which DNAs are extracted from the
CC adherent-causing microorganisms for analysis to reveal the microbial
CC phase or predominant or specific microorganism, e.g. slime, after
CC comparison. The method is used for screening and selecting anti-microbial
CC agents particularly for controlling and treating slimes in papermaking
CC industry, which can also be applied in monitoring anti-microbial effect,
CC analysis of product adherents. The present sequence is a Filamentous
CC fungi 18S rDNA partial sequence isolated by the method of the invention
XX
SQ Sequence 501 BP; 146 A; 100 C; 122 G; 133 T; 0 U; 0 Other;

Query Match 100.0%; Score 23; DB 6; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAACTCTAGAG 23
DB 98 GGATAACCGTGGTAACTCTAGAG 120

Search completed: January 9, 2006, 18:38:54
Job time : 341 secs

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Db      |||||
87 GGATAACCGTGGTAATTCCTAGAG 109

RESULT 2
AU012452
LOCUS      154 bp mRNA linear EST 03-AUG-1998
DEFINITION Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc06817, mRNA sequence.
ACCESSION AU012452
VERSION AU012452.1 GI:3357361
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
1 (bases 1 to 154)
/note="Vector: pBlueScript SK(-); Site 1: EcoRI; Site 2:
XhoI; supplier: Tankalev; Flower buds and flowers were
taken from greenhouse plants (4-8 wks old, TA496). They
were immediately frozen in liquid nitrogen and then
size-separated while remaining frozen."
REFERENCE Morimyo,M. and Mita,K.
AUTHORS Identification of expressed sequence tags of Schizosaccharomyces
pombe
TITLE Unpublished (1998)
JOURNAL Contact: Mitsuoki Morimyo
COMMENT Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
1. .154
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/db_xref="taxon:4896"
/strain="972"
/clone="spc06817"
/sex="h minus"
/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
ORIGIN
Query Match 100.0%; Score 23; DB 1; Length 154;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
|||||
Db 87 GGATAACCGTGGTAATTCCTAGAG 109

RESULT 3
AW217889
LOCUS      191 bp mRNA linear EST 18-MAY-2001
DEFINITION tomato flower buds, anthesis, Cornell University
Lycopersicon esculentum cDNA clone cTOD1C1 similar to Ipomoea
hederacea 18S ribosomal RNA gene, mRNA sequence.
ACCESSION AW217889
VERSION AW217889.1 GI:6528763
KEYWORDS EST.
SOURCE Lycopersicon esculentum (Solanum lycopersicum)
ORGANISM Lycopersicon esculentum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 191)
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
REFERENCE van der Hoeven,R.S., Bezzerides,J.L., Matern,A.L., Holt,I.E.,
Liang,F., Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn.S.,
Ronning,C.M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and
Tankalev,S.D.
AUTHORS Generation of ESTs from tomato flower tissue
TITLE Unpublished (1998)
JOURNAL Contact: Mitsuoki Morimyo
COMMENT Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
1. .191
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/db_xref="taxon:4896"
/strain="972"
/clone="spc01233"
/sex="h minus"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
ORIGIN
Query Match 100.0%; Score 23; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
|||||
Db 51 GGATAACCGTGGTAATTCCTAGAG 73

RESULT 4
AU006980/c
LOCUS      193 bp mRNA linear EST 31-JUL-1998
DEFINITION Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc01233, mRNA sequence.
ACCESSION AU006980
VERSION AU006980.1 GI:3343438
KEYWORDS EST.
SOURCE Schizosaccharomyces pombe (fission yeast)
ORGANISM Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomycetes.
1 (bases 1 to 193)
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
REFERENCE Morimyo,M. and Mita,K.
AUTHORS Identification of expressed sequence tags of Schizosaccharomyces
pombe
TITLE Unpublished (1998)
JOURNAL Contact: Mitsuoki Morimyo
COMMENT Genome Research Group
National Institute of Radiological Sciences
9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
Email: morimyo@nirs.go.jp.
Location/Qualifiers
1. .193
/organism="Schizosaccharomyces pombe"
/mol_type="mRNA"
/db_xref="taxon:4896"
/strain="972"
/clone="spc01233"
/sex="h minus"
/note="Vector: M13mp19; The cDNA library of
Schizosaccharomyces pombe was prepared by cloning cDNA
into the SmaI site of M13mp19 DNA and the direction of DNA
sequences was not always from 5' to 3'. The cDNA data of
Schizosaccharomyces pombe are available for searching on
the World Wide Web. (URL, http://www.nirs.go.jp)"
ORIGIN
Query Match 100.0%; Score 23; DB 1; Length 191;
Best Local Similarity 100.0%; Pred. No. 0.62;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
|||||
Db 51 GGATAACCGTGGTAATTCCTAGAG 73
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Query Match 100.0%; Score 23; DB 1; Length 193;
 Best Local Similarity 100.0%; Pred. No. 0.63; Mismatches 0; Indels 0; Gaps 0;
 Matches 23; Conservative 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
 |||||
 DB 80 GGATAACCGTGGTAATTCCTAGAG 58

RESULT 5
 AU009944 200 bp mRNA linear EST 31-JUL-1998
 LOCUS AU009944 Schizosaccharomyces pombe late log phase cDNA
 DEFINITION Schizosaccharomyces pombe cDNA clone spc00704, mRNA sequence.

ACCESSION AU009944
 VERSION AU009944.1 GI:3346624
 KEYWORDS EST.

SOURCE Schizosaccharomyces pombe (fission yeast)
 ORGANISM Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.

REFERENCE 1 (bases 1 to 200)
 AU009944 Morimyo.M. and Mita.K.

AUTHORS Identification of expressed sequence tags of Schizosaccharomyces

TITLE pombe

JOURNAL Unpublished (1998)

COMMENT Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.

FEATURES
 source Location/Qualifiers

1..200 /organism="Schizosaccharomyces pombe"

/mol_type="mRNA"

/strain="972"

/db_xref="taxon:4896"

/clone="spc00704"

/sex="h minus"

/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of
 Schizosaccharomyces pombe was prepared by cloning cDNA
 into the SmaI site of M13mp19 DNA and the direction of DNA
 sequences was not always from 5' to 3'. The cDNA data of
 Schizosaccharomyces pombe are available for searching on
 the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 200;
 Best Local Similarity 100.0%; Pred. No. 0.63;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
 |||||
 DB 121 GGATAACCGTGGTAATTCCTAGAG 143

RESULT 6
 AU010607 208 bp mRNA linear EST 31-JUL-1998
 LOCUS AU010607 Schizosaccharomyces pombe late log phase cDNA
 DEFINITION Schizosaccharomyces pombe cDNA clone spc10128, mRNA sequence.

ACCESSION AU010607
 VERSION AU010607.1 GI:3347287
 KEYWORDS EST.

SOURCE Schizosaccharomyces pombe (fission yeast)

ORGANISM Schizosaccharomyces pombe
 Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 Schizosaccharomycetales; Schizosaccharomycetaceae;
 Schizosaccharomycetes.

REFERENCE 1 (bases 1 to 208)

AUTHORS

TITLE

JOURNAL

COMMENT

Morimyo.M. and Mita,K.
 Identification of expressed sequence tags of Schizosaccharomyces
 pombe
 Unpublished (1998)
 Contact: Mitsuoki Morimyo
 Genome Research Group
 National Institute of Radiological Sciences
 9-1, Anagawa-4-chome, Inage-ku, Chiba, Chiba 263-8555, Japan
 Email: morimyo@nirs.go.jp.

FEATURES

source

1..208 /organism="Schizosaccharomyces pombe"

/mol_type="mRNA"

/strain="972"

/db_xref="taxon:4896"

/clone="spc10128"

/sex="h minus"

/clone_lib="Schizosaccharomyces pombe late log phase cDNA"
 /note="Vector: M13mp19; The cDNA library of
 Schizosaccharomyces pombe was prepared by cloning cDNA
 into the SmaI site of M13mp19 DNA and the direction of DNA
 sequences was not always from 5' to 3'. The cDNA data of
 Schizosaccharomyces pombe are available for searching on
 the World Wide Web. (URL, http://www.nirs.go.jp)"

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 208;

Best Local Similarity 100.0%; Pred. No. 0.63;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23

|||||

DB 129 GGATAACCGTGGTAATTCCTAGAG 151

RESULT 7

AL749833

LOCUS

DEFINITION

AL749833 AS Pinus pinaster cDNA clone AS01F05 similar to 18S, mRNA

sequence.

AL749833 216 bp mRNA linear EST 20-JUN-2002

AL749833.1 GI:21491067

VERSION

KEYWORDS

SOURCE

ORGANISM

Pinus pinaster

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus.

1 (bases 1 to 216)

Frigerio,J. and Plomion,C.

Identification of water-deficit responsive genes in Maritime pine

(Pinus pinaster Ait.) using an EST approach

Unpublished (2002)

CONTACT: Frigerio JM

Genetique et Amelioration 69

INRA

route d'Arcachon 33612 Cestas CEDEX France

Email: Frigerio@pierrot.inra.fr

Seq primer: T3.

Location/Qualifiers

1..216

/organism="Pinus pinaster"

/mol_type="mRNA"

/db_xref="taxon:71647"

/clone="AS01F05"

/dev_stage="shoot"

/lab_host="SOLR"

/clone_lib="AS"

/note="Vector: Uni-ZAP XR; ecotype: Landes; The library

was made from the aerial part (above the collar) of 6

weeks old seedlings grown in hydroponic conditions. A

three weeks drought stress treatment was applied by

lowering the osmotic potential of the nutrient solution to

-0.45 MPa using 170 g/l of polyethylene glycol as an osmoticum. A mixture of genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms and mass-excised to form a pBluescript phagemid"

ORIGIN
Query Match 100.0%; Score 23; DB 1; Length 216;
Best Local Similarity 100.0%; Pred. No. 0.64; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 1 GGATAACCGTGGTAATCTAGAG 23
|||||
Db 117 GGATAACCGTGGTAATCTAGAG 139

RESULT 8
AW791051
LOCUS
DEFINITION
D00369-R Lambda Zap, Stratagene Blumeria graminis f. sp. hordei EST 01-MAY-2001
CDNA clone D00369 similar to hypothetical protein 2, mRNA sequence.
AW791051
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Blumeria graminis f. sp. hordei
Blumeria graminis f. sp. hordei
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomyces;
Erysipales; Erysiphaceae; Blumeria.
REFERENCE
1 (bases 1 to 222)
AUTHORS
Thomas S.W., Rasmussen, S.W., Glaring, M.A., Rouster, J.A. and Oliver, R.P.

TITLE
Gene identification in the fungal pathogen Blumeria graminis by expressed sequence tag analysis
JOURNAL
COMMENT
Unpublished (2000)
Contact: Rasmussen, S.W.
Department of Yeast Genetics
Carlsberg Laboratory
10 Gl. Carlsbergvej, DK-2500, Copenhagen, Denmark
Tel: 45 3327 5230
Fax: 45 3327 4766
Email: swr@erc.dk
High quality sequence stop: 222
POLYA=No.

FEATURES
source
1..222
/organism="Blumeria graminis f. sp. hordei"
/mol_type="mRNA"
/db_xref="taxon:62688"
/clone="D00369"
/cell_type="conidia"
/lab_host="Hordeum vulgare"
/clone_lib="Lambda Zap, Stratagene"

ORIGIN
Query Match 100.0%; Score 23; DB 1; Length 222;
Best Local Similarity 100.0%; Pred. No. 0.64; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

QY 1 GGATAACCGTGGTAATCTAGAG 23
|||||
Db 173 GGATAACCGTGGTAATCTAGAG 195

RESULT 9
CF945579
LOCUS
DEFINITION
TrEST-A2815 TrEST-A Hypocrea jecorina cDNA clone Tr-A2815 5', mRNA
CF945579
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Hypocrea jecorina

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocremycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 230)
Chambergo, F.S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P.,
Ferreira, J.R.Jr., Abrahao-Neto, J., Farah, J.P.S. and El-Dorri, H.
Elucidation of the metabolic fate of glucose in the filamentous
fungus Trichoderma reesei using expressed sequence tag (EST)
analysis and cDNA microarrays
J. Biol. Chem. 277 (16), 13983-13988 (2002)
11825887
Contact: El-Dorri, Hamza
Department of Biochemistry
Institute of Chemistry, University of Sao Paulo
Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,
BRASIL
Tel: (55) 11-38183848
Fax: (55) 11-38183848
Email: dorri@iq.usp.br
PCR Primers
FORWARD: Universal M13 forward primer
BACKWARD: Universal M13 reverse primer
Plate: 30 row: C column: 7
Seq primer: M13 reverse primer
High quality sequence stop: 229
POLYA=No.

FEATURES

source

Location/Qualifiers
1..230
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM9414 (ATCC26921)"
/db_xref="taxon:51453"
/clone="Tr-A2815"
/sex="Asexual"
/tissue_type="Mycelia"
/dev_stage="18 hr Glycerol-grown culture"
/lab_host="E. coli SOLR cells (kanamycin resistant)"
/clone_lib="TrEST-A"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; anamorph-Trichoderma reesei; Cloned
unidirectionally, 5' end of the cDNA cloned into EcoRI
site of pBluescript. Primer: Oligo (dT). Average insert
size: 1.2 kb; Uni-ZAP XR Vector system -5' adaptor
sequence: 5'GAATTCGGCAGG3' -3' adaptor sequence:
5'CTCGAGTTTTTTTTTTTTTTTT3'."

ORIGIN

Query Match 100.0%; Score 23; DB 7; Length 230;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATCTAGAG 23

Db 132 GGATAACCGTGGTAATCTAGAG 154

RESULT 10

CF945596

LOCUS

DEFINITION

TrEST-A2885 TrEST-A Hypocrea jecorina cDNA clone Tr-A2885 5', mRNA

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

FEATURES

source

Location/Qualifiers

1..230

/organism="Hypocrea jecorina"

/mol_type="mRNA"

/strain="QM9414 (ATCC26921)"

/db_xref="taxon:51453"

/clone="Tr-A2815"

/sex="Asexual"

/tissue_type="Mycelia"

/dev_stage="18 hr Glycerol-grown culture"

/lab_host="E. coli SOLR cells (kanamycin resistant)"

/clone_lib="TrEST-A"

/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2: XhoI; anamorph-Trichoderma reesei; Cloned unidirectionally, 5' end of the cDNA cloned into EcoRI site of pBluescript. Primer: Oligo (dT). Average insert size: 1.2 kb; Uni-ZAP XR Vector system -5' adaptor sequence: 5'GAATTCGGCAGG3' -3' adaptor sequence: 5'CTCGAGTTTTTTTTTTTTTTTT3'."

JOURNAL
PUBMED
COMMENT

J. Biol. Chem. 277 (16), 13983-13988 (2002)
11825887
Contact: El-Dorriy, Hamza
Department of Biochemistry
Institute of Chemistry. University of Sao Paulo
Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,
BRASIL
Tel: (55) 11-38183848
Fax: (55) 11-38183848
Email: dorry@iq.usp.br

PCR Primers
FORWARD: Universal M13 forward primer
BACKWARD: Universal M13 reverse primer
Plate: 31 row: A column: 5
Seq primer: M13 reverse primer
High quality sequence stop: 232
POLYA=No.

FEATURES

source

Location/Qualifiers

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1..233
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM9414 (ATCC26921)"
/db_xref="taxon:51453"
/clone="Tr-A2885"
/sex="Asexual"
/tissue_type="Mycelia"
/dev_stage="18 hr Glycerol-grown culture"
/lab_host="E. coli SOLR cells (kanamycin resistant)"
/clone_lib="TrEST-A"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; anamorph=Trichoderma reesei; Cloned
unidirectionally, 5' end of the cDNA cloned into EcoRI
site of pBluescript. Primer: Oligo (dT). Average insert
size: 1.2 kb; Uni-ZAP XR Vector system -5' adaptor
sequence: 5'GAATTCGGCAGG3' -3' adaptor sequence:
5'CTCGAGTTTTTTTTTTTTTTT3'"
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ORIGIN

Query Match 100.0%; Score 23; DB 7; Length 233;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23

Db 125 GGATAACCGTGGTAATCTAGAG 147

RESULT 11
LOCUS CF945185 236 bp mRNA linear EST 19-NOV-2003
DEFINITION TrEST-A2863 TrEST-A Hypocrea jecorina cDNA clone Tr-A2863 5', mRNA
sequence.
ACCESSION CF945185
VERSION CF945185.1 GI:38445705
KEYWORDS EST.
SOURCE Hypocrea jecorina (anamorph: Trichoderma reesei)
ORGANISM Hypocrea jecorina
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
1 (bases 1 to 236)
Chamberg, P.S., Bonaccorsi, E.D., Ferreira, A.J.S., Ramos, A.S.P.,
Ferreira, J.R.Jr., Abrahao-Neto, J., Farah, J.P.S. and El-Dorriy, H.
Elucidation of the metabolic fate of glucose in the filamentous
fungus Trichoderma reesei using expressed sequence tag (EST)
analysis and cDNA microarrays
J. Biol. Chem. 277 (16), 13983-13988 (2002)
11825887
Contact: El-Dorriy, Hamza
Department of Biochemistry
Institute of Chemistry. University of Sao Paulo
Avenida Professor Lineu Prestes, 748, Sao Paulo, SP, 05508-900,
BRASIL
Tel: (55) 11-38183848

Fax: (55) 11-38183848
Email: dorry@iq.usp.br

PCR Primers
FORWARD: Universal M13 forward primer
BACKWARD: Universal M13 reverse primer
Plate: 30 row: G column: 7
Seq primer: M13 reverse primer
High quality sequence stop: 230
POLYA=No.

FEATURES

source

Location/Qualifiers

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1..236
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/mol_type="mRNA"
/strain="QM9414 (ATCC26921)"
/db_xref="taxon:51453"
/clone="Tr-A2863"
/sex="Asexual"
/tissue_type="Mycelia"
/dev_stage="18 hr Glycerol-grown culture"
/lab_host="E. coli SOLR cells (kanamycin resistant)"
/clone_lib="TrEST-A"
/note="Vector: pBluescript SK(+); Site 1: EcoRI; Site 2:
XhoI; anamorph=Trichoderma reesei; Cloned
unidirectionally, 5' end of the cDNA cloned into EcoRI
site of pBluescript. Primer: Oligo (dT). Average insert
size: 1.2 kb; Uni-ZAP XR Vector system -5' adaptor
sequence: 5'GAATTCGGCAGG3' -3' adaptor sequence:
5'CTCGAGTTTTTTTTTTTTTTT3'"
```

ORIGIN

Query Match 100.0%; Score 23; DB 7; Length 236;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23

Db 125 GGATAACCGTGGTAATCTAGAG 147

RESULT 12

AA532319

LOCUS

DEFINITION

AA532319

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

254 bp mRNA linear EST 23-AUG-2000
CPEST.449 uniZAPCpIOMAsporolib3 Cryptosporidium parvum cDNA 5',
mRNA sequence.
AA532319 1 GI:2276511
EST.
Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 254)
Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genome: an
expressed sequence tag and genome survey sequence analysis
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
10717299
Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
Francisco
Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' to
the insert, to correct miscalled bases and assign uncalled (N)
bases throughout the sequence, and to terminate when base-calling
became ambiguous.
Seq primer: M13 reverse
High quality sequence stop: 254.
Location/Qualifiers
1..254

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/organism="Cryptosporidium parvum"
/mol_type="mRNA"
/strain="IOWA"
/db_xref="taxon:5807"
/dev_stage="sporozoite"
/lab_host="E. coli XL1 Blue MRF' Kan"
/clone_lib="uniZAPc10WASporolib3"
/notes="Vector: UniZAP XR; Site 1: EcoR I; Site 2: Xho I;
The C. parvum cDNA library was prepared by Drs. Norman J.
Plentzsek, Michael J. Arrowood, Susan B. Slemenda, and Jan
R. Mead at the Centers for Disease Control and Prevention
(Atlanta, Georgia). Poly A+ RNA was separated from total
C. parvum RNA using the Poly(A) Quik mRNA Isolation Kit
from Stratagene. Directional cDNA was synthesized by
first-strand priming with a Xho I-oligo d(T)
linker-primer, second-stranding with RNase H and DNA
polymerase I, ligation of EcoR I linkers, and digestion
with Xho I, all using the Stratagene ZAP-cDNA synthesis
kit. The cDNA was cloned into the EcoR I and Xho I sites
of Lambda Uni-ZAP XR vector; the unamplified library was
>95% recombinant and contained 3.8 X 10(6) independent
clones. PCR analysis of 20 random clones indicated that
the average insert size was ca. 1.1 kb."

ORIGIN
Query Match 100.0%; Score 23; DB 1; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCAG 23
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Db 114 GGATAACCGTGGTAATTCAG 136

RESULT 13
CD029939 256 bp mRNA linear EST 07-MAY-2003
LOCUS mgmk014XB02f.b pmk1 in pBluescriptII sk(-) plasmid Magnaporthe
DEFINITION Gristea cDNA clone mgmk014XB02 5', mRNA sequence.
ACCESSION CD029939
VERSION CD029939.1 GI:30411775
KEYWORDS EST.
SOURCE Magnaporthe grisea (anamorph: Pyricularia grisea)
ORGANISM Magnaporthe grisea
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS Sordariomycetes incertae sedis; Magnaporthaceae; Magnaporthe.
1 (bases 1 to 256)
TITLE Ebbole,D.J., Yuan,J., Thomas,T.L., Bobrowicz,P., Lu,G.,
Bhatterai,K. and Dean,R.A.
JOURNAL Expressed sequence tags from the rice blast fungus, Magnaporthe
COMMENT Grisea
Unpublished (2002)
Contact: Ebbole DJ
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg, MS2132, College Station, TX 77843-2132, USA
Tel: 979 845 4831
Fax: 979 845 6483
Email: d-ebbole@tamu.edu
Chromatogram file of this sequence is available, see contact
person:Best nr hit (April. 22, 2003) ref|XP_284680.1| similar to
hypothetical protein 2 (rRNA externa. . . 31 4.0
PCR Primers
FORWARD: T3 primer
BACKWARD: T7 primer
Plate: mgmk014 row: B column: 02
Seq primer: T3.
FEATURES
source
location/Qualifiers
1..256
/organism="Magnaporthe grisea"
/mol_type="mRNA"
/strain="NN95"
/db_xref="taxon:148305"

/clone="mgmk014XB02"
/sex="Mat1-1 hermaphrodite"
/cell_type="germinated conidia"
/clone_lib="pmk1 in pBluescriptII sk(-) plasmid"
/notes="Vector: pBluescriptSK; Site 1: EcoRI; Site 2: XhoI;
Conidia germinated in hydrophobic surface membrane in 27C
for 12 hours. NN95 is a hygromycin phosphotransferase gene
replacement of the PMK1 MAP kinase gene in the Guy11
strain background (Xu and Hamer, 1996. Genes & Dev.
10:2696). Sequences were processed by one of two methods.
Where a full-length alignment to the M. grisea genome
sequence was available, the EST sequence was trimmed
according to the alignment, otherwise sequence quality was
assessed using phredPhrap version 991019 and trimmed
according to phd files (0.05) and for vector seqs."

ORIGIN
Query Match 100.0%; Score 23; DB 6; Length 256;
Best Local Similarity 100.0%; Pred. No. 0.65;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCAG 23
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Db 109 GGATAACCGTGGTAATTCAG 131

RESULT 14
AI398053 269 bp mRNA linear EST 08-FEB-1999
LOCUS NCSC2C4T7 Subtracted Conidial Neurospora crassa cDNA clone SC2C4
DEFINITION 3', mRNA sequence.
ACCESSION AI398053
VERSION AI398053.1 GI:4241138
KEYWORDS EST.
SOURCE Neurospora crassa
ORGANISM Neurospora crassa
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
1 (bases 1 to 269)
TITLE Nelson,M.A., Kang,S., Braun,E.B., Crawford,M.E., Dolan,P.L.,
Leonard,P.M., Mitchell,J., Armijo,A.M., Bean,L., Blueyes,E.,
Cushing,T., Ertett,A., Fleharty,M., Gorman,M., Judson,K.,
Miller,R., Ortega,J., Pavlova,I., Perea,J., Todisco,S.,
Trujillo,R., Valentine,J., Wells,A., Werner-Washburne,M., Yazzie,S.
and Natvig,D.O.
JOURNAL Expressed sequences from conidial, mycelial, and sexual stages of
COMMENT Neurospora crassa
Fungal Genet. Biol. 21, 348-363 (1997)
9290248
Contact: Natvig,D.O./Nelson,M.A.
Department of Biology
University of New Mexico
Castetter Hall, Albuquerque, NM 87131, USA
Tel: 505 277 3411
Fax: 505 277 0304
Email: ngp@biology.unm.edu.
FEATURES
source
location/Qualifiers
1..269
/organism="Neurospora crassa"
/mol_type="mRNA"
/strains="74-OR23-IV A (FGSC 2489)"
/db_xref="taxon:5141"
/clone="SC2C4"
/sex="Mating Type A"
/tissue_type="Conidia"
/dev_stage="Germinating conidia"
/lab_host="E. coli"
/clone_lib="Subtracted Conidial"
/notes="Vector: pBluescript SK (-); Site 1: EcoRI; Site 2:
XhoI; mRNA isolated from germinating conidia, grown in lx
Vogel's, 2% sucrose for 4.5 hours. cDNA directionally
cloned into pBluescript SK(-) using the Uni-ZAP XR vector
system (Stratagene, La Jolla, CA). Previously identified

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Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match	100.0%	Score 23	DB 1	Length 269
Best Local Similarity	100.0%	Pred. No. 0.66		
Matches 23	Conservative	0	Mismatches 0	Indels 0
Gaps				0

Search completed: January 9, 2006, 21:16:55
Job time : 2480 secs

BUB38475	BUB38475.	278 bp	linear	mrna	EST 06-MAY-2003
LOCUS	mgcw009xe23f.b	RCW Lambda zap	Express Library	Magnaporthe grisea	
DEFINITION	cdna clone mgcw009xe23 5'			mrna sequence.	

ACCESSION
NUMBER B0638475.1 GI:23350801

KEYWORDS
EST.

SOURCE
Magnetaporthe grisea (anamorph: Pyricularia grisea)

ORGANISM
Magnetaporthe grisea

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariomycetes incertae sedis; Magnaporthaceae; Magnetaporthe.

1 (BASES 1 TO 276)
 Ebbola, D.J., Yuan, J., Thomas, T.L., Bobrowicz, P., Lu, G.,
 Bhatte, K. and Dean, R.A.

JOURNAL
Unpublished (2002)

CONTACT: LORRAE DO
Department of Plant Pathology & Microbiology
Texas A&M University
Peterson Bldg. MS2132, College Station, TX 77843-2132, USA

Fax: 979 845 6483
 Email: d-ebol@camu.edu
 Chromatogram file of this sequence is available, see contact
 person; Best nr hit (April. 22, 2003) gb|EAA2131.1| hypothetical
 protein [Plasmodium voelii voelii] 35 0.21

FORWARD: T5 primer
BACKWARD: T7 primer

Plate: MGCW003
Seq primer: T3

FEATURES	Location/Qualifiers
1	278

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/organism="Magnaporthe oryzae"
/seq_type="cdna"
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/strain="CP987"
```

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/clone="mgcw009xE23"
```

```
/tissue_type="Mycelium"
```

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/clone_lib="RCW Lambda Zap Express Library"
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Express; Site_1: EcoRI; Site_2: XhoI; Day 5

post-inoculation mRNAs prepared from Magnaporthe grisea grown at 23°C in the dark with constant gyratory shaking 100 rpm in Vogel's minimal medium containing 0.5% isolated

rice cell walls as the sole carbon source. Library

provided by Sheng-Cheng Wu. Sequences were processed by

provided by ordering among the sequences. The results of the alignment to the one of two methods. Where a full-length alignment to the one of two methods.

M. grisea genome sequence was available, the EST sequence

M. grisea genome sequence was available, the reference sequence was trimmed according to the alignment; otherwise sequence

was claimed according to the arrangement; otherwise sequences
quality was assessed using phredphrap version 991019 and

quality was assessed using `phredmap` version 3.0.13 and trimmed according to phd files (0.05) and for vector

Trimmed according to pnd and litter (0.05) and tot vector
cccc "

[illegible]

Query Match

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 18:17:01 ; Search time 102.5 Seconds
(without alignments)
398.867 Million cell updates/sec

Title: US-09-954-586-46

Perfect score: 23

Sequence: 1 ggataaccgtggaattcttagag 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B COMB.seq:*

5: /cgn2_6/ptodata/1/ina/H COMB.seq:*

6: /cgn2_6/ptodata/1/ina/PCTUS COMB.seq:*

7: /cgn2_6/ptodata/1/ina/PP COMB.seq:*

8: /cgn2_6/ptodata/1/ina/RE COMB.seq:*

9: /cgn2_6/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	100.0	444	2	US-08-093-144-5
2	23	100.0	444	2	US-08-093-144-6
3	23	100.0	446	2	US-08-093-144-4
4	23	100.0	570	3	US-09-533-559-1021
5	23	100.0	617	3	US-09-533-559-3436
6	23	100.0	1750	3	US-08-949-770-1
7	23	100.0	1788	2	US-08-867-820A-1
8	23	100.0	2055	3	US-10-121-740-3
9	23	100.0	2089	3	US-10-121-740-1
10	23	100.0	2293	3	US-09-645-073-1
11	21.4	93.0	25	3	US-09-396-196G-761
12	21.4	93.0	40	2	US-07-720-587A-2
13	21.4	93.0	312	3	US-09-270-767-10466
14	21.4	93.0	1665	3	US-09-805-127-7
15	21.4	93.0	22118	3	US-09-815-981A-5
16	20	87.0	1747	2	US-08-327-516-1
17	20	87.0	1747	3	US-09-281-766-1
18	20	87.0	1747	3	US-09-612-858-1
19	20	87.0	1747	3	US-09-957-995A-1
20	19.8	86.1	568	3	US-09-533-553-4668
21	19.8	86.1	703	3	US-08-998-416-178
22	19.8	86.1	706	3	US-08-998-416-814
23	19.8	86.1	709	3	US-08-998-416-281
24	19.8	86.1	712	3	US-08-998-416-910

25	19.8	86.1	717	3	US-08-998-416-602
26	19.8	86.1	723	3	US-08-998-416-952
27	19.8	86.1	1608	2	US-08-899-371-2
28	19.8	86.1	1759	3	US-10-052-092-25
29	19.8	86.1	1776	3	US-09-350-710B-1
30	18.4	80.0	1744	2	US-07-879-647A-25
31	18.4	80.0	1744	2	US-07-879-584A-25
32	18.4	80.0	1744	2	US-07-879-470A-25
33	18.4	80.0	1744	2	US-07-879-644A-25
34	18.4	80.0	1744	2	US-07-879-640A-25
35	18.4	80.0	1744	2	US-07-879-594A-25
36	18.4	80.0	1744	2	US-07-879-469A-25
37	18.4	80.0	1747	2	US-07-879-647A-29
38	18.4	80.0	1747	2	US-07-879-584A-29
39	18.4	80.0	1747	2	US-07-879-470A-29
40	18.4	80.0	1747	2	US-07-879-644A-29
41	18.4	80.0	1747	2	US-07-879-640A-29
42	18.4	80.0	1747	2	US-07-879-594A-29
43	18.4	80.0	1747	2	US-07-879-469A-29
44	18.4	80.0	1747	3	US-09-015-259-1
45	18.4	80.0	1747	3	US-09-015-259-2

ALIGNMENTS

RESULT 1

US-08-093-144-5

; Sequence 5, Application US/08093144

; Patent No. 5434048

; GENERAL INFORMATION:

; APPLICANT: SIMON, LUC

; APPLICANT: LALONDE, MAURICE

; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF

; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI

; NUMBER OF SEQUENCES: 21

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

; STREET: Eleventh Floor, 1615 L. Street, N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20036-5601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Tape

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/093,144

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA: US 07/745,192

; APPLICATION NUMBER: 15-AUG-1991

; FILING DATE: 15-AUG-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Hymo, Lawrence A.

; REGISTRATION NUMBER: 19, 057

; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 861-3000

; TELEFAX: (202) 822-0944

; TELEX: 6714627 CUSH

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 444 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

US-08-093-144-5

Query Match 100.0%; Score 23; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.094;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATCTAGAG 23
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Db 33 GGATAACCGTGGTAATCTAGAG 55

RESULT 2

US-08-093-144-6
; Sequence 6, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,192
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-093-144-6

Query Match 100.0%; Score 23; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATCTAGAG 23
|||||
Db 33 GGATAACCGTGGTAATCTAGAG 55

RESULT 3

US-08-093-144-4
; Sequence 4, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN

; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,192
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-093-144-4

Query Match 100.0%; Score 23; DB 2; Length 446;
Best Local Similarity 100.0%; Pred. No. 0.094;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATCTAGAG 23
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Db 32 GGATAACCGTGGTAATCTAGAG 54

RESULT 4

US-09-533-559-1021/c
; Sequence 1021, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849, 200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1021
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)...(570)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-1021

Query Match 100.0%; Score 23; DB 3; Length 570;

Best Local Similarity 100.0%; Pred. No. 0.096; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mismatches 0;

Qy 1 GGATAACCGTGGTAATTCTAGAG 23
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Db 422 GGATAACCGTGGTAATTCTAGAG 400

RESULT 5

US-09-533-559-3436
; Sequence 3436, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533.559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273.623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3436
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Fusarium venenatum
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(617)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-3436

Query Match 100.0%; Score 23; DB 3; Length 617;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCTAGAG 23
|||||
Db 125 GGATAACCGTGGTAATTCTAGAG 147

RESULT 6

US-08-949-770-1
; Sequence 1, Application US/08949770
; Patent No. 6063604
; GENERAL INFORMATION:
; APPLICANT: Wick, James F.
; APPLICANT: Mueller, Reinhold
; APPLICANT: Blasak, Michele
; APPLICANT: Wilkosz, Richard K.
; TITLE OF INVENTION: Target Nucleic Acid Sequence Amplification
; Patent No. 6063604
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,770

; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,045
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochoplen, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 28003/33045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1750 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: /= "18s rRNA gene of Cryptosporidium"
; OTHER INFORMATION: parvum"
US-08-949-770-1

Query Match 100.0%; Score 23; DB 3; Length 1750;
Best Local Similarity 100.0%; Pred. No. 0.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCTAGAG 23
|||||
Db 141 GGATAACCGTGGTAATTCTAGAG 163

RESULT 7

US-08-867-820A-1
; Sequence 1, Application US/08867820A
; Patent No. 5891685
; GENERAL INFORMATION:
; APPLICANT: YAMAGISHI Masahiro
; APPLICANT: TAKAI Yukie
; APPLICANT: MIKAWA Takashi
; APPLICANT: HARA Mari
; APPLICANT: UEDA Makoto
; APPLICANT: OHARA Akiko
; TITLE OF INVENTION: METHOD FOR PRODUCING ESTER OF (S)- -HALOGENATED- -HYDROXYBUTY
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WENDEROTH, LIND & PONACK, L.L.P.
; STREET: 2033 K Street, N.W., Suite 800
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867.820A
; FILING DATE: June 3, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee Cheng
; REGISTRATION NUMBER: 40,949
; REFERENCE/DOCKET NUMBER: 1416/OP574US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-721-8200
; TELEFAX: 202-721-8250
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1788 base pairs

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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: Genomic DNA
; ORIGINAL SOURCE:
; ORGANISM: Candida albicans
; STRAIN: MUCL29800
US-08-867-820A-1

Query Match      100.0%; Score 23; DB 2; Length 1788;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 141 GGATAACCGTGGTAATTCCTAGAG 163

RESULT 8
US-10-121-740-3
; Sequence 3, Application US/10121740
; Patent No. 6911338
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; FILE REFERENCE: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Muscador roseus
US-10-121-740-3

Query Match      100.0%; Score 23; DB 3; Length 2055;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 124 GGATAACCGTGGTAATTCCTAGAG 146

RESULT 9
US-10-121-740-1
; Sequence 1, Application US/10121740
; Patent No. 6911338
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; FILE REFERENCE: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2089
; TYPE: DNA
; ORGANISM: Muscador albus
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US-10-121-740-1

Query Match      100.0%; Score 23; DB 3; Length 2089;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 137 GGATAACCGTGGTAATTCCTAGAG 159

RESULT 10
US-09-645-073-1
; Sequence 1, Application US/09645073
; Patent No. 6287800
; GENERAL INFORMATION:
; APPLICANT: Lee, May
; APPLICANT: Galazzo, Jorge
; TITLE OF INVENTION: Production of High Titers of Gibberellins GA4 and GA7
; FILE REFERENCE: L02-01NP
; CURRENT APPLICATION NUMBER: US/09/645,073
; CURRENT FILING DATE: 2000-08-25
; PRIOR APPLICATION NUMBER: US 60/151,770
; PRIOR FILING DATE: 1999-08-31
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 2293
; TYPE: DNA
; ORGANISM: Gibberella fujikuroi
US-09-645-073-1

Query Match      100.0%; Score 23; DB 3; Length 2293;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 117 GGATAACCGTGGTAATTCCTAGAG 139

RESULT 11
US-09-396-196G-761
; Sequence 761, Application US/09396196G
; Patent No. 6821724
; GENERAL INFORMATION:
; APPLICANT: Michael Mittmann
; APPLICANT: David Mack
; APPLICANT: David Lockhart
; APPLICANT: Affymetrix, Inc.
; TITLE OF INVENTION: Methods of Genetic Analysis
; FILE REFERENCE: 3101.1
; CURRENT APPLICATION NUMBER: US/09/396,196G
; CURRENT FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/100,678
; PRIOR FILING DATE: 1998-09-17
; NUMBER OF SEQ ID NOS: 127806
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 761
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-396-196G-761

Query Match      93.0%; Score 21.4; DB 3; Length 25;
Best Local Similarity 95.7%; Pred. No. 0.45;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 1 GGATAACCGTGGTAATTCCTAGAG 23
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RESULT 12
US-07-720-587A-2/C
; Sequence 2, Application US/07720587A
; Patent No. 5352579
; GENERAL INFORMATION:
; APPLICANT: Curt L. Millman
; TITLE OF INVENTION: NUCLEIC ACIDS PROBES
; TITLE OF INVENTION: TO HISTOPLASMA CAPSULATUM
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 611 West Sixth Street
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90017
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.0)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07720,587A
; FILING DATE: 19910628
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: including application
; PRIOR APPLICATION DATA: described below:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warburg, Richard J.
; REGISTRATION NUMBER: 32,327
; REFERENCE/DOCKET NUMBER: 193/121
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 489-1600
; TELEFAX: (213) 955-0440
; TELEX: 67-3510
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 40
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-720-587A-2

Query Match 93.0%; Score 21.4; DB 2; Length 40;
Best Local Similarity 95.7%; Pred. No. 0.47;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 29 GGATAACCGTGGTAATTCCTAGAG 7

RESULT 13
US-09-270-767-10466
; Sequence 10466, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 10466
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10466
; LENGTH: 312
; TYPE: DNA
; ORGANISM: Drosophila melanogaster
; US-09-270-767-10466

Query Match 93.0%; Score 21.4; DB 3; Length 22118;
Best Local Similarity 95.7%; Pred. No. 0.76;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 9787 GGATAACCGTGGTAATTCCTAGAG 9809

Search completed: January 9, 2006, 21:20:28
Job time : 105.5 secs
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Query Match 93.0%; Score 21.4; DB 3; Length 312;
Best Local Similarity 95.7%; Pred. No. 0.55;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 142 GGATAACCGTGGTAATTCCTAGAG 164

RESULT 14
US-09-805-127-7
; Sequence 7, Application US/09805127
; Patent No. 6653119
; GENERAL INFORMATION:
; APPLICANT: BIO MEDIATION TECHNOLOGIE, INC.
; TITLE OF INVENTION: WHITE ROT FUNGI AND METHOD FOR DECOMPOSING DIOXINS USING THEM
; FILE REFERENCE: WKO-101ECT
; CURRENT APPLICATION NUMBER: US/09/805,127
; CURRENT FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: JP 1998-260707
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1665
; TYPE: DNA
; ORGANISM: White rod fungus MZ-340
; US-09-805-127-7

Query Match 93.0%; Score 21.4; DB 3; Length 1665;
Best Local Similarity 95.7%; Pred. No. 0.62;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 88 GGATAACCGTGGTAATTCCTAGAG 110

RESULT 15
US-09-815-981A-5
; Sequence 5, Application US/09815981A
; Patent No. 6936469
; GENERAL INFORMATION:
; APPLICANT: de Jong, Gary
; APPLICANT: Vandebyl, Sandra
; TITLE OF INVENTION: METHODS FOR DELIVERING NUCLEIC ACID
; FILE REFERENCE: 24601-416B
; CURRENT APPLICATION NUMBER: US/09/815,981A
; CURRENT FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 22118
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-815-981A-5

Query Match 93.0%; Score 21.4; DB 3; Length 22118;
Best Local Similarity 95.7%; Pred. No. 0.76;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 9787 GGATAACCGTGGTAATTCCTAGAG 9809
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model
Run on: January 9, 2006, 19:55:45 ; Search time 517 Seconds
(without alignments)
367.883 Million cell updates/sec

Title: US-09-954-586-46
Perfect score: 23
Sequence: 1 ggataaccgtggaattcttagag 23
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0
Searched: 9793542 seqs, 4134689005 residues
Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA Main:
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2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq.*
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9: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq.*
10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	100.0	23	3	US-09-954-695-46
2	23	100.0	23	3	US-09-954-695-52
3	23	100.0	23	3	US-09-954-695-58
4	23	100.0	23	3	US-09-954-695-64
5	23	100.0	23	3	US-09-954-586-46
6	23	100.0	23	3	US-09-954-586-52
7	23	100.0	23	3	US-09-954-586-58
8	23	100.0	23	3	US-09-954-586-64
9	23	100.0	32	3	US-09-954-695-29
10	23	100.0	32	3	US-09-954-695-33
11	23	100.0	32	3	US-09-954-695-37
12	23	100.0	32	3	US-09-954-695-41
13	23	100.0	32	3	US-09-954-586-29
14	23	100.0	32	3	US-09-954-586-33
15	23	100.0	32	3	US-09-954-586-37
16	23	100.0	32	3	US-09-954-586-41
17	23	100.0	384	9	US-10-950-009-47
18	23	100.0	501	7	US-10-466-016-6
19	23	100.0	538	9	US-10-950-009-48
20	23	100.0	540	9	US-10-950-009-49
21	23	100.0	570	8	US-10-653-047-1021
22	23	100.0	617	8	US-10-653-047-3436
23	23	100.0	685	6	US-10-094-097B-112

24	23	100.0	1228	9	US-10-483-439-1	Sequence 1, Appli
25	23	100.0	2055	6	US-10-121-740-3	Sequence 3, Appli
26	23	100.0	2055	7	US-10-623-432-3	Sequence 3, Appli
27	23	100.0	2055	10	US-11-131-659-3	Sequence 1, Appli
28	23	100.0	2089	6	US-10-121-740-1	Sequence 1, Appli
29	23	100.0	2089	7	US-10-623-432-1	Sequence 1, Appli
30	23	100.0	2089	10	US-11-131-659-1	Sequence 1, Appli
31	21.4	93.0	25	8	US-10-719-900-602235	Sequence 602235,
32	21.4	93.0	25	9	US-10-809-189-761	Sequence 761, App
33	21.4	93.0	135	8	US-10-357-930-12550	Sequence 12550, A
34	21.4	93.0	135	8	US-10-357-930-14189	Sequence 14189, A
35	21.4	93.0	136	8	US-10-357-930-14412	Sequence 14412, A
36	21.4	93.0	161	6	US-10-264-049-1193	Sequence 1193, Ap
37	21.4	93.0	174	8	US-10-357-930-5020	Sequence 5020, Ap
38	21.4	93.0	183	8	US-10-357-930-33712	Sequence 33712, A
39	21.4	93.0	187	8	US-10-357-930-12578	Sequence 12578, A
40	21.4	93.0	187	8	US-10-357-930-12586	Sequence 12586, A
41	21.4	93.0	192	6	US-10-125-968-281	Sequence 281, App
42	21.4	93.0	199	8	US-10-357-930-12553	Sequence 12553, A
43	21.4	93.0	265	3	US-09-925-299-402	Sequence 402, App
44	21.4	93.0	265	3	US-09-925-299-402	Sequence 402, App
45	21.4	93.0	298	10	US-11-060-867-93	Sequence 93, Appli

ALIGNMENTS

RESULT 1
US-09-954-695-46
; Sequence 46, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-46

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGTAACTTCTAG 23

DB 1 GGATAACCGTGTAACTTCTAG 23

RESULT 2
US-09-954-695-52
; Sequence 52, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695

; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-52

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.18;
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23
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Db 1 GGAUAACCGUGGUUAUUCUAGAG 23

RESULT 3

US-09-954-695-58/c
; Sequence 58, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 58
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-58

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23
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Db 23 GGATAACCGTGGTAATTTCTAGAG 1

RESULT 4

US-09-954-695-64/c
; Sequence 64, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 64
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-64

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23
|||||:-|||:-|||:-|||:-|||
Db 23 GGATAACCGTGGTAATTTCTAGAG 1

RESULT 5

US-09-954-586-46
; Sequence 46, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-46

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTTCTAGAG 23
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Db 1 GGATAACCGTGGTAATTTCTAGAG 23

RESULT 6

US-09-954-586-52
; Sequence 52, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
US-09-954-586-52

OTHER INFORMATION: Synthetic Construct
US-09-954-586-52

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 73.9%; Pred. No. 0.18;
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23
|||:||||:|:|:|:|:|:|
Db 1 GGAUAACCGUGUAUUCUAGAG 23

RESULT 7
US-09-954-586-58/c
; Sequence 58, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954.586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 58
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-58

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18; Length 23;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23
|||:||||:|:|:|:|:|:|
Db 23 GGATAACCGTGGTAATCTAGAG 1

RESULT 8
US-09-954-586-64/c
; Sequence 64, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954.586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 64
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-64

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.18;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23
|||:||||:|:|:|:|:|:|
Db 23 GGATAACCGTGGTAATCTAGAG 1

RESULT 9
US-09-954-695-29
; Sequence 29, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954.695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 29
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-29

Query Match 100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.19; Length 32;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23
|||:||||:|:~|:~|:~|:~|:~|
Db 1 GGATAACCGTGGTAATCTAGAG 23

RESULT 10
US-09-954-695-33
; Sequence 33, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; TITLE OF INVENTION: CRYPTOSPORIDIUM ORGANISMS IN A TEST SAMPLE
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954.695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 33
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-33

Query Match 100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 73.9%; Pred. No. 0.19;
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATCTAGAG 23
|||:||||:|:~|:~|:~|:~|:~|
Db 1 GGAUAACCGUGUAUUCUAGAG 23

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RESULT 11
US-09-954-695-37/c
; Sequence 37, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-37

Query Match      100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 32 GGATAACCGTGGTAATTCCTAGAG 10

RESULT 12
US-09-954-695-41/c
; Sequence 41, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-41

Query Match      100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 32 GGATAACCGTGGTAATTCCTAGAG 10

RESULT 13
US-09-954-586-29
; Sequence 29, Application US/09954586
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; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-29

Query Match      100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 1 GGATAACCGTGGTAATTCCTAGAG 23

RESULT 14
US-09-954-586-33
; Sequence 33, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 32
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-33

Query Match      100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 73.9%; Pred. No. 0.19;
Matches 17; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCCTAGAG 23
Db 1 GGATAACCGUGGUAUUCUAGAG 23

RESULT 15
US-09-954-586-37/c
; Sequence 37, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
```

;; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
;; TITLE OF INVENTION: CRYPTOSPORIDIUM PARVUM ORGANISMS IN A TEST SAMPLE

;; FILE REFERENCE: GPL16-03.UT

;; CURRENT APPLICATION NUMBER: US/09/954,586

;; CURRENT FILING DATE: 2001-09-11

;; PRIOR APPLICATION NUMBER: US 60/232,028

;; PRIOR FILING DATE: 2000-09-12

;; NUMBER OF SEQ ID NOS: 69

;; SOFTWARE: PatentIn version 3.1

;; SEQ ID NO 37

;; LENGTH: 32

;; TYPE: DNA

;; ORGANISM: Artificial Sequence

;; FEATURE:

;; OTHER INFORMATION: Synthetic Construct

US-09-954-586-37

Query Match 100.0%; Score 23; DB 3; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.19;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTCTAGAG 23
|||
Db 32 GGATAACCGTGGTAATTCTAGAG 10

Search completed: January 10, 2006, 00:04:32
Job time : 518 secs

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November 2005

Published Applications Nucleic Acid and Published Applications Amino Acid database searches now generate two sets of results each. The Published Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published Applications New databases; older published applications make up the Published Applications Main databases.

Searches run against Nucleic Acid Published Applications produce two sets of results, with the extensions **.rppbm** (Published Applications NA_Main) and **.rnpbm** (Published Applications NA_New). Searches run against Amino Acid Published Applications produce two sets of results, with the extensions **.rapbm** (Published Applications AA_Main) and **.rapbn** (Published Applications AA_New).

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 21:17:07 ; Search time 215 Seconds
(without alignments)
77.993 Million cell updates/sec

Title: US-09-954-586-46

Perfect score: 23
Sequence: 1 ggataaccgtggaattcttagag 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
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3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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10: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	23	100.0	1732	6	US-10-519-379-1
2	21.4	93.0	1874	7	US-11-136-527-4032
3	21.4	93.0	1920	7	US-11-136-527-174864
4	21.4	93.0	1920	7	US-11-136-527-174865
5	21.4	93.0	1920	7	US-11-136-527-174866
6	21.4	93.0	1969	6	US-10-775-169-210
7	21.4	93.0	1969	6	US-10-947-249-33
8	21.4	93.0	59590	7	US-11-117-187-187
9	16.6	72.2	1391	6	US-10-750-185-31917
10	16.6	72.2	1391	6	US-10-750-623-31917
11	16.6	72.2	1542	6	US-10-873-528-205
12	16.6	72.2	1542	6	US-10-873-528-245
13	16.4	71.3	3688	6	US-10-750-185-30025
14	16.4	71.3	3688	6	US-10-750-623-30025
15	15.8	68.7	19	8	US-11-101-244-1440038
16	15.8	68.7	19	9	US-11-083-784-1440038
17	15.8	68.7	235033	7	US-11-157-389-1
18	15.8	68.7	237326	7	US-11-157-389-2
19	15.6	67.8	201	6	US-10-995-561-24091
20	15.6	67.8	600	6	US-10-750-185-1120
21	15.6	67.8	600	6	US-10-750-623-1120
22	15.6	67.8	159138	6	US-10-995-561-13230
23	15.4	67.0	1983	6	US-10-750-185-50579

c	24	15.4	67.0	1983	6	US-10-750-623-50579	Sequence 50579, A
	25	15.2	66.1	913	6	US-10-750-185-38513	Sequence 38513, A
	26	15.2	66.1	913	6	US-10-750-623-38513	Sequence 38513, A
	27	15.2	66.1	1128	6	US-10-750-185-41157	Sequence 41157, A
	28	15.2	66.1	1128	6	US-10-750-623-41157	Sequence 41157, A
	29	15.2	66.1	1144	7	US-11-136-527-4058	Sequence 4058, Ap
c	30	15.2	66.1	1144	7	US-11-136-527-8154	Sequence 8154, Ap
c	31	15.2	66.1	1525	6	US-10-750-185-40363	Sequence 40363, A
	32	15.2	66.1	1525	6	US-10-750-623-40363	Sequence 40363, A
c	33	15.2	66.1	2444	7	US-11-136-527-3546	Sequence 3546, Ap
c	34	15.2	66.1	96583	7	US-11-117-187-203	Sequence 203, App
c	35	15.2	66.1	105550	6	US-10-995-561-13235	Sequence 13235, A
	36	15	65.2	294	6	US-10-467-657-5153	Sequence 5153, Ap
	37	15	65.2	967	6	US-10-750-185-27830	Sequence 27830, A
	38	15	65.2	967	6	US-10-750-623-27830	Sequence 27830, A
c	39	15	65.2	1627	6	US-10-750-185-28345	Sequence 28345, A
c	40	15	65.2	1627	6	US-10-750-623-28345	Sequence 28345, A
c	41	15	65.2	1771	6	US-10-750-185-61743	Sequence 61743, A
c	42	15	65.2	1771	6	US-10-750-623-61743	Sequence 61743, A
c	43	15	65.2	2699	7	US-11-064-246-6	Sequence 6, Appli
c	44	15	65.2	2699	7	US-11-064-246-6	Sequence 8, Appli
c	45	15	65.2	129021	7	US-11-117-187-202	Sequence 202, App

ALIGNMENTS

RESULT 1
US-10-519-379-1
; Sequence 1, Application US/10519379
; Publication No. US20050255126A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI DENKA Co., Ltd.
; TITLE OF INVENTION: New microorganism and method for producing aglucan by the new
; TITLE OF INVENTION: microorganism
; FILE REFERENCE: A0301
; CURRENT APPLICATION NUMBER: US/10/519,379
; CURRENT FILING DATE: 2004-12-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Aureobasidium pullulans ADK-34
US-10-519-379-1

Query Match 100.0%; Score 23; DB 6; Length 1732;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGATAACCGTGGTAATCTTAGAG 23
Db 102 GGATAACCGTGGTAATCTTAGAG 124

RESULT 2
US-11-136-527-4032
; Sequence 4032, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4032
; LENGTH: 1874
; TYPE: DNA
; ORGANISM: Rattus norvegicus

US-11-136-527-4032

Query Match 93.0%; Score 21.4; DB 7; Length 1874;
Best Local Similarity 95.7%; Pred. No. 0.091;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATACCGTGGTAATCTAG 23
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Db 145 GGATAACTGGGTAATCTAG 167

RESULT 3

US-11-136-527-174864
; Sequence 174864, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 174864
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-174864

Query Match 93.0%; Score 21.4; DB 7; Length 1920;
Best Local Similarity 95.7%; Pred. No. 0.091;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATACCGTGGTAATCTAG 23
||||| ||||||| ||||||| ||||||| |||||||
Db 154 GGATAACTGGGTAATCTAG 176

RESULT 4

US-11-136-527-174865
; Sequence 174865, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 174865
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-174865

Query Match 93.0%; Score 21.4; DB 7; Length 1920;
Best Local Similarity 95.7%; Pred. No. 0.091;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATACCGTGGTAATCTAG 23
||||| ||||||| ||||||| ||||||| |||||||
Db 154 GGATAACTGGGTAATCTAG 176

RESULT 5

US-11-136-527-174866

; Sequence 174866, Application US/11136527
; Publication No. US20050287570A1
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Mounts, William M
; TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
; FILE REFERENCE: 031896-041000 (AM101086)
; CURRENT APPLICATION NUMBER: US/11/136,527
; CURRENT FILING DATE: 2005-05-25
; PRIOR APPLICATION NUMBER: US 60/574,294
; PRIOR FILING DATE: 2005-05-26
; NUMBER OF SEQ ID NOS: 362830
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 174866
; LENGTH: 1920
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-11-136-527-174866

Query Match 93.0%; Score 21.4; DB 7; Length 1920;
Best Local Similarity 95.7%; Pred. No. 0.091;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATACCGTGGTAATCTAG 23
||||| ||||||| ||||||| ||||||| |||||||
Db 154 GGATAACTGGGTAATCTAG 176

RESULT 6

US-10-775-169-210
; Sequence 210, Application US/10775169
; Publication No. US20050287532A9
; GENERAL INFORMATION:

; APPLICANT: Wyeth
; APPLICANT: Burczynski, Michael
; APPLICANT: Twine, Natalie
; APPLICANT: Dornier, Andrew
; APPLICANT: Trepicchio, William
; TITLE OF INVENTION: Method for Monitoring Drug Activities In Vivo
; FILE REFERENCE: AM101080 (031896-013000)
; CURRENT APPLICATION NUMBER: US/10/775,169
; CURRENT FILING DATE: 2004-02-11
; NUMBER OF SEQ ID NOS: 5278
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 210
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (57)..(61)
; OTHER INFORMATION: Each "n" represents a nucleotide selected from a, t, g or c, or
; OTHER INFORMATION: contains no nucleotide.
US-10-775-169-210

Query Match 93.0%; Score 21.4; DB 6; Length 1969;
Best Local Similarity 95.7%; Pred. No. 0.091;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATACCGTGGTAATCTAG 23
||||| ||||||| ||||||| ||||||| |||||||
Db 246 GGATAACTGGGTAATCTAG 268

RESULT 7

US-10-947-249-33
; Sequence 33, Application US/10947249
; Publication No. US20050287541A1
; GENERAL INFORMATION:

; APPLICANT: Akira NAKAGAWARA
; APPLICANT: Miki OHIRA
; APPLICANT: Shin ISHII
; APPLICANT: Takeshi GOTO

```

; APPLICANT: Hiroyuki KUBO
; APPLICANT: Takahiro HIRATA
; APPLICANT: Yasuko YOSHIDA
; APPLICANT: Saichi YAMADA
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Meth
; TITLE OF INVENTION: Predicting the Prognosis of Neuroblastoma
; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (57)..(61)
; OTHER INFORMATION: n is a, t, g or c
US-10-947-249-33

Query Match 93.0%; Score 21.4; DB 6; Length 1969;
Best Local Similarity 95.7%; Pred. No. 0.091;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTTCTAGAG 23
Db 246 GGATAACTGGTAAATTTCTAGAG 268

RESULT 8
US-11-117-187-187
; Sequence 187, Application US/11117187
; Publication No. US20050286560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVEN, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD-309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 187
; LENGTH: 59590
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (2521)..(57768)
; OTHER INFORMATION: N = A, C, G, or T/U
US-11-117-187-187

Query Match 93.0%; Score 21.4; DB 7; Length 59590;
Best Local Similarity 95.7%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTTCTAGAG 23
Db 42882 GGATAACCGTAGTAATTTCTAGAG 42904

RESULT 9
US-10-750-185-31917/c
; Sequence 31917, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M

```

```

; APPLICANT: Hiroyuki KUBO
; APPLICANT: Takahiro HIRATA
; APPLICANT: Yasuko YOSHIDA
; APPLICANT: Saichi YAMADA
; TITLE OF INVENTION: Microarray for Predicting the Prognosis of Neuroblastoma and Meth
; TITLE OF INVENTION: Predicting the Prognosis of Neuroblastoma
; FILE REFERENCE: 117007
; CURRENT APPLICATION NUMBER: US/10/947,249
; CURRENT FILING DATE: 2004-09-23
; PRIOR APPLICATION NUMBER: US 60/505,614
; PRIOR APPLICATION NUMBER: 2003-09-25
; NUMBER OF SEQ ID NOS: 200
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 1969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (57)..(61)
; OTHER INFORMATION: n is a, t, g or c
US-10-947-249-33

Query Match 93.0%; Score 21.4; DB 6; Length 1969;
Best Local Similarity 95.7%; Pred. No. 0.091;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTTCTAGAG 23
Db 246 GGATAACTGGTAAATTTCTAGAG 268

RESULT 8
US-11-117-187-187
; Sequence 187, Application US/11117187
; Publication No. US20050286560A1
; GENERAL INFORMATION:
; APPLICANT: PREUSS, DAPHNE
; APPLICANT: COPENHAVEN, GREGORY
; TITLE OF INVENTION: PLANT ARTIFICIAL CHROMOSOME COMPOSITIONS AND METHODS
; FILE REFERENCE: ARCD-309US
; CURRENT APPLICATION NUMBER: US/11/117,187
; CURRENT FILING DATE: 2005-04-28
; PRIOR APPLICATION NUMBER: US/09/531,120
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/125,219
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 187
; LENGTH: 59590
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (2521)..(57768)
; OTHER INFORMATION: N = A, C, G, or T/U
US-11-117-187-187

Query Match 93.0%; Score 21.4; DB 7; Length 59590;
Best Local Similarity 95.7%; Pred. No. 0.17;
Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGATAACCGTGGTAATTTCTAGAG 23
Db 42882 GGATAACCGTAGTAATTTCTAGAG 42904

RESULT 9
US-10-750-185-31917/c
; Sequence 31917, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M

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; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PMC/P21129W0
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 205
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-205

Query Match          72.2%; Score 16.6; DB 6; Length 1542;
Best Local Similarity 82.6%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCAG 23
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Db 336 GGATAAACGTTTAAATCTAAG 358

RESULT 12
US-10-873-528-245
; Sequence 245, Application US/10873528
; Publication No. US20050276814A1
; GENERAL INFORMATION:
; APPLICANT: Microbial Technics Limited
; APPLICANT: Gilbert, Christophe FG
; APPLICANT: Hansbro, Philip M
; TITLE OF INVENTION: Proteins
; FILE REFERENCE: PMC/P21129W0
; CURRENT APPLICATION NUMBER: US/10/873,528
; CURRENT FILING DATE: 2004-06-23
; PRIOR APPLICATION NUMBER: US/09/769,787
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: GB 9816337.1
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: US 60/125164
; PRIOR FILING DATE: 1999-03-19
; NUMBER OF SEQ ID NOS: 388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 245
; LENGTH: 1542
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-873-528-245

Query Match          72.2%; Score 16.6; DB 6; Length 1542;
Best Local Similarity 82.6%; Pred. No. 29;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGATAACCGTGGTAATTCAG 23
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Db 336 GGATAAACGTTTAAATCTAAG 358

RESULT 13
US-10-750-185-30025/c
; Sequence 30025, Application US/10750185
; Publication No. US200502603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; CURRENT APPLICATION NUMBER: US/11/101,244

US-10-750-185-30025
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30025
; LENGTH: 3688
; TYPE: DNA
; ORGANISM: Bovine 19866881048613
US-10-750-185-30025

Query Match          71.3%; Score 16.4; DB 6; Length 3688;
Best Local Similarity 94.4%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 ATAACCGTGGTAATTCCTA 20
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Db 2394 ATAACCATGGTAATTCCTA 2377

RESULT 14
US-10-750-623-30025/c
; Sequence 30025, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 30025
; LENGTH: 3688
; TYPE: DNA
; ORGANISM: Bovine 19866881048613
US-10-750-623-30025

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Best Local Similarity 94.4%; Pred. No. 44;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 2394 ATAACCATGGTAATTCCTA 2377

RESULT 15
US-11-101-244-1440038/c
; Sequence 1440038, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
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; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 1440038
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-1440038

Query Match      68.7%; Score 15.8; DB 8; Length 19;
Best Local Similarity 89.5%; Pred. No. 34;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db      19 AACAGTGGTAATCTATAG 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

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Perfect score: 23
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Searched: 5983141 seqs, 28421725653 residues

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3: gb_env.*
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10: gb_sts.*
11: gb_sy.*
12: gb_un.*
13: gb_vi.*
14: gb_ttg.*
15: gb_pl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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C 2	23	100.0	23	6	AX421407	Sequence
C 3	23	100.0	23	6	AX421413	Sequence
C 4	23	100.0	23	6	AX421419	Sequence
C 5	23	100.0	413	2	AY508962	Cryptosporo
C 6	23	100.0	415	2	AY508963	Cryptosporo
C 7	23	100.0	600	2	AF262332	Cryptosporo
C 8	23	100.0	646	2	DQ003721	Cryptosporo
C 9	23	100.0	660	2	AF316630	Cryptosporo
C 10	23	100.0	665	2	AF316631	Cryptosporo
C 11	23	100.0	704	2	CP18RRNA1	Cryptosporo
C 12	23	100.0	712	2	DQ067569	Cryptosporo
C 13	23	100.0	715	2	AF262326	Cryptosporo
C 14	23	100.0	744	2	AY268582	Cryptosporo
C 15	23	100.0	748	2	AY268583	Cryptosporo
C 16	23	100.0	755	2	AY504517	Cryptosporo
C 17	23	100.0	769	2	DQ067565	Cryptosporo
C 18	23	100.0	770	2	AY741305	Cryptosporo

C 19	23	100.0	770	2	DQ067566	Cryptosporo
C 20	23	100.0	771	2	AY120910	Cryptosporo
C 21	23	100.0	771	2	AY120911	Cryptosporo
C 22	23	100.0	771	2	AY120912	Cryptosporo
C 23	23	100.0	771	2	AY587166	Cryptosporo
C 24	23	100.0	774	2	CPA493071	Cryptosporo
C 25	23	100.0	774	2	CPA493546	Cryptosporo
C 26	23	100.0	775	3	AY737576	Cryptosporo
C 27	23	100.0	776	2	AY504513	Cryptosporo
C 28	23	100.0	776	2	CME493073	Cryptosporo
C 29	23	100.0	776	2	CME493203	Cryptosporo
C 30	23	100.0	776	2	CME493204	Cryptosporo
C 31	23	100.0	776	2	CME493205	Cryptosporo
C 32	23	100.0	776	2	CME493206	Cryptosporo
C 33	23	100.0	776	2	CME493207	Cryptosporo
C 34	23	100.0	776	2	CME493549	Cryptosporo
C 35	23	100.0	777	2	CPA493074	Cryptosporo
C 36	23	100.0	777	2	CPA493075	Cryptosporo
C 37	23	100.0	777	2	CPA493080	Cryptosporo
C 38	23	100.0	777	2	CPA493084	Cryptosporo
C 39	23	100.0	777	2	CPA493085	Cryptosporo
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C 44	23	100.0	777	2	CPA493198	Cryptosporo
C 45	23	100.0	777	2	CPA493200	Cryptosporo

ALIGNMENTS

RESULT 1
AX421401/c
LOCUS AX421401 23 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 47 from Patent WO0222890.
ACCESSION AX421401
VERSION AX421401.1 GI:21524796

SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.

REFERENCE 1

AUTHORS

TITLE

JOURNAL

FEATURES

source

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/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

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Best Local Similarity 100.0%; Pred. No. 17;
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Qy 1 CCGTAAAGTTATTATGAGTCACC 23

Db 23 CCGTAAAGTTATTATGAGTCACC 1

RESULT 2

AX421407/c

LOCUS AX421407 23 bp RNA linear PAT 18-JUN-2002

DEFINITION Sequence 53 from Patent WO0222890.

ACCESSION AX421407

VERSION AX421407.1 GI:21524802

KEYWORDS

SOURCE synthetic construct

ORGANISM synthetic construct

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other sequences; artificial sequences.
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REFERENCE      Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
AUTHORS        Compositions, methods and kits for determining the presence of
TITLE          cryptosporidium organisms in a test sample
JOURNAL        Patent: WO 0222890-A 53 21-MAR-2002;
FEATURES       Gen-Probe Incorporated (US)
source         Location/Qualifiers
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 23 CCGTAAAGTTATTATGAGTCACC 1

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LOCUS          AX421413          23 bp      DNA      linear      PAT 18-JUN-2002
DEFINITION    Sequence 59 from Patent WO0222890.
ACCESSION     AX421413
VERSION       AX421413.1 GI:21524808
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE        Compositions, methods and kits for determining the presence of
JOURNAL      cryptosporidium organisms in a test sample
JOURNAL      Patent: WO 0222890-A 59 21-MAR-2002;
JOURNAL      Gen-Probe Incorporated (US)
FEATURES     Location/Qualifiers
1. .23
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/db_xref="taxon:32630"

ORIGIN
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
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Db 1 CCGTAAAGTTATTATGAGTCACC 23

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LOCUS          AX421419          23 bp      RNA      linear      PAT 18-JUN-2002
DEFINITION    Sequence 65 from Patent WO0222890.
ACCESSION     AX421419
VERSION       AX421419.1 GI:21524814
KEYWORDS      .
SOURCE        synthetic construct
ORGANISM      other sequences; artificial sequences.
REFERENCE     1
AUTHORS       Cunningham,M.M., Stull,P.D. and Weisburg,W.G.
TITLE        Compositions, methods and kits for determining the presence of
JOURNAL      cryptosporidium organisms in a test sample
JOURNAL      Patent: WO 0222890-A 65 21-MAR-2002;
JOURNAL      Gen-Probe Incorporated (US)
FEATURES     Location/Qualifiers
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Query Match      100.0%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
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Db 1 CCGTAAAGTTATTATGAGTCACC 23

RESULT 5
AX508962/c
LOCUS          AX508962/c        413 bp      DNA      linear      INV 25-FEB-2004
DEFINITION    Cryptosporidium parvum strain Fox8 18S ribosomal RNA gene, partial
sequence.
ACCESSION     AY508962
VERSION       AY508962.1 GI:42716333
KEYWORDS      .
SOURCE        Cryptosporidium parvum
ORGANISM      Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
REFERENCE     1 (bases 1 to 413)
AUTHORS       Nagano,Y., Finn,M.B., Lowery,C.J., Murphy,T., McCorry,K.A.,
Crothers,E., Watabe,M., Rao,J.R., Dooley,J.S.G., Rooney,P.J.,
Matsuda,M. and Moore,J.E.
TITLE        Cryptosporidium parvum 18S rRNA partial gene sequence
JOURNAL      Unpublished
REFERENCE     2 (bases 1 to 413)
AUTHORS       Finn,M.B., Lowery,C.J., Nagano,Y., Moore,J.E. and Dooley,J.S.G.
TITLE        Direct Submission
JOURNAL      Submitted (18-DEC-2003) Department of Bacteriology, Northern
Ireland Public Health Laboratory, Belfast City Hospital, Lisburn
Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK
FEATURES     Location/Qualifiers
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/strains="Fox3"
/isolation_source="fecal material from a fox"
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/country="Ireland"
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/product="18S ribosomal RNA"

rRNA
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Best Local Similarity 100.0%; Pred. No. 7.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
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Db 30 CCGTAAAGTTATTATGAGTCACC 8

RESULT 6
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LOCUS          AX508963/c        415 bp      DNA      linear      INV 25-FEB-2004
DEFINITION    Cryptosporidium parvum strain Fox8 18S ribosomal RNA gene, partial
sequence.
ACCESSION     AY508963
VERSION       AY508963.1 GI:42716334
KEYWORDS      .
SOURCE        Cryptosporidium parvum
ORGANISM      Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
REFERENCE     1 (bases 1 to 415)
AUTHORS       Nagano,Y., Finn,M.B., Lowery,C.J., Murphy,T., McCorry,K.A.,

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Crothers,E., Watabe,M., Rao,J.R., Dooley,J.S.G., Rooney,P.J.,
 Matsuda,M. and Moore,J.E.
 Cryptosporidium parvum 18S rRNA partial gene sequence
 Unpublished
 2 (bases 1 to 415)
 Finn,M.B., Lowery,C.J., Nagano,Y., Moore,J.E. and Dooley,J.S.G.
 Direct Submission
 Submitted (18-DEC-2003) Department of Bacteriology, Northern
 Ireland Public Health Laboratory, Belfast City Hospital, Lisburn
 Road, Belfast, Co. Antrim BT9 7AD, Northern Ireland, UK
 Location/Qualifiers
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 /organism="Cryptosporidium parvum"
 /mol_type="genomic DNA"
 /strain="Fox8"
 /isolation_source="fecal material from a fox"
 /db_xref="taxon:5807"
 /country="Ireland"
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 /product="18S ribosomal RNA"
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 Best Local Similarity 100.0%; Pred. No. 7.9;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 CCGTAAAGTTATTATGAGTCACC 23
 Db 32 CCGTAAAGTTATTATGAGTCACC 10
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 RESULT 7
 AF262332/c
 LOCUS
 DEFINITION
 Cryptosporidium sp. isolate N small subunit ribosomal RNA gene,
 partial sequence.
 AF262332
 AF262332.1 GI:11761742
 Cryptosporidium sp.
 Cryptosporidium sp.
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Cryptosporidiidae; Cryptosporidium.
 1 (bases 1 to 600)
 Xiao,L., Alderisio,K., Limor,J., Royer,M. and Lal,A.A.
 Identification of species and sources of Cryptosporidium oocysts in
 storm waters with a small-subunit rRNA-based diagnostic and
 genotyping tool
 Appl. Environ. Microbiol. 66 (12), 5492-5498 (2000)
 11097935
 2 (bases 1 to 600)
 Xiao,L., Alderisio,K., Limor,J.R., Royer,M. and Lal,A.A.
 Direct Submission
 Submitted (02-MAY-2000) Division of Parasitic Diseases, Centers for
 Disease Control and Prevention, 4770 Buford Highway, F-12,
 Chamblee, GA 30341, USA
 Location/Qualifiers
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 /mol_type="genomic DNA"
 /isolate="N"
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 Db 62 CCGTAAAGTTATTATGAGTCACC 40
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 Cryptosporidium parvum strain bovine 18S ribosomal RNA gene,
 partial sequence.
 DQ003721
 DQ003721.1 GI:62911041
 Cryptosporidium parvum
 Cryptosporidium parvum
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Cryptosporidiidae; Cryptosporidium.
 1 (bases 1 to 646)
 Azadpour-Keeley,A. and Caldwell,M.
 Evaluation of Cryptosporidium oocysts and Giardia cysts in a
 watershed reservoir
 Unpublished
 2 (bases 1 to 646)
 Azadpour-Keeley,A.
 Direct Submission
 Submitted (11-APR-2005) EPA/ORD/NRMRL, GWERD, 919 Kerr Research
 Dr., Ada, OK 74820, USA
 Location/Qualifiers
 1. .646
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 Best Local Similarity 100.0%; Pred. No. 7.1;
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 Db 61 CCGTAAAGTTATTATGAGTCACC 39
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 LOCUS
 DEFINITION
 Cryptosporidium sp. BDI 18S ribosomal RNA gene, partial sequence.
 AF316630
 AF316630.1 GI:12744417
 Cryptosporidium sp. BDI
 Cryptosporidium sp. BDI
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Cryptosporidiidae; Cryptosporidium.
 1 (bases 1 to 660)
 Morgan,U.M., Monis,P.T., Xiao,L., Limor,J., Sulaiman,I., Raidal,S.,
 O'Donoghue,P., Gasser,R., Murray,A., Fayer,R., Blagburn,B.L.,
 Lal,A.A. and Thompson,A.R.C.
 Molecular and phylogenetic characterisation of Cryptosporidium from
 birds
 Int. J. Parasitol. 31 (3), 289-296 (2001)
 11226456
 2 (bases 1 to 660)
 Morgan,U.M., Monis,P.T. and Xiao,L.
 Direct Submission
 Submitted (26-OCT-2000) Division of Veterinary and Biomedical
 Science, Murdoch University, Murdoch Drive, Perth, WA 6150,
 Australia
 Location/Qualifiers
 FEATURES

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1. .660
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rRNA

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QY 1 CCGTAAAGTTATTATGAGTCACC 23
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Db 213 CCGTAAAGTTATTATGAGTCACC 191

RESULT 10
AF316631/c
LOCUS
DEFINITION Cryptosporidium sp. Q1 18S ribosomal RNA gene, partial sequence.
ACCESSION AF316631
VERSION AF316631.1 GI:12744418
KEYWORDS
SOURCE
ORGANISM
Cryptosporidium sp. Q1
Cryptosporidium sp. Q1
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
REFERENCE
1 (bases 1 to 665)
Morgan,U.M., Monis,P.T., Xiao,L., Limor,J., Sulaiman,I., Raidal,S.,
O'Donoghue,P., Gasser,R., Murray,A., Fayer,R., Blagburn,B.L.,
Lal,A.A. and Thompson,A.R.C.
Molecular and phylogenetic characterisation of Cryptosporidium from
birds
Int. J. Parasitol. 31 (3), 289-296 (2001)
11226456
2 (bases 1 to 665)
Morgan,U.M., Monis,P.T. and Xiao,L.
Direct Submission
Submitted (26-OCT-2000) Division of Veterinary and Biomedical
Science, Murdoch University, Murdoch Drive, Perth, WA 6150,
Australia
LOCATION/Qualifiers
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/isolate="Q1"
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<1. .>665
/product="18S ribosomal RNA"

rRNA

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Best Local Similarity 100.0%; Pred. No. 7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 11
CP188RNA1/c
LOCUS
DEFINITION Cryptosporidium parvum 18S ribosomal RNA gene, partial sequence.
ACCESSION AF162429
VERSION AF162429.1 GI:5916184
KEYWORDS
SEGMENT
1 of 2
Cryptosporidium parvum

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ORGANISM
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 704)
Blears,M.J., Pokorny,N.J., Carreno,R.A., Chen,S., De Grandis,S.A.,
Lee,H. and Trevors,J.T.
DNA fingerprinting of Cryptosporidium parvum isolates using
amplified fragment length polymorphism (AFLP)
J. Parasitol. 86 (4), 838-841 (2000)
10958466
2 (bases 1 to 704)
Pokorny,N.J.
Direct Submission
Submitted (24-JUN-1999) Environmental Biology, University of
Guelph, Edmund C. Bovey Building, Guelph, ON N1G 2W1, Canada
LOCATION/Qualifiers
source
1. .704
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/country="USA; Louisiana"

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Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
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RESULT 12
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LOCUS
DEFINITION
Cryptosporidium parvum strain vlr200443 small subunit ribosomal RNA
gene, partial sequence.
DQ067569
DQ067569.1 GI:67527112
ACCESSION
VERSION
KEYWORDS
SOURCE
Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 712)
Kang,G., Dheepa,M., Jayandhran,B., Ramani,S. and Ward,H.D.
Multi-locus genotyping of Cryptosporidium species from HIV-infected
individuals with and without diarrhea in southern India
Unpublished
2 (bases 1 to 712)
Kang,G., M.D., Jayandhran,B., Ramani,S. and Ward,H.D.
Direct Submission
Submitted (19-MAY-2005) GI Sciences, Christian Medical College, Ida
Scudder Road, Vellore, TN 632004, India
LOCATION/Qualifiers
source
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Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 CCGTAAAGTTATTATGAGTCACC 7

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RESULT 13
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LOCUS
DEFINITION
Cryptosporidium sp. isolate KK small subunit ribosomal RNA gene,
partial sequence.
ACCESSION
AF262326
VERSION
AF262326.1 GI:11761736
KEYWORDS
Cryptosporidium sp.
SOURCE
Cryptosporidium sp.
ORGANISM
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
REFERENCE
1 (bases 1 to 715)
Xiao,L., Alderisio,K., Limor,J., Royer,M. and Lal,A.A.
Identification of species and sources of Cryptosporidium oocysts in
storm waters with a small-subunit rRNA-based diagnostic and
genotyping tool
Appl. Environ. Microbiol. 66 (12), 5492-5498 (2000)
JOURNAL
PUBMED
11097935
REFERENCE
2 (bases 1 to 715)
Xiao,L., Alderisio,K., Limor,J.R., Royer,M. and Lal,A.A.
Direct Submission
TITLE
Submitted (02-MAY-2000) Division of Parasitic Diseases, Centers for
Disease Control and Prevention, 4770 Buford Highway, F-12,
Chamblee, GA 30341, USA
JOURNAL
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Location/Qualifiers
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genotype: W9"
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/product="small subunit ribosomal RNA"

rRNA

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Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTATGAGTCACC 23
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Db 62 CCGTAAAGTTATTATGAGTCACC 40

RESULT 14
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LOCUS
DEFINITION
Cryptosporidium parvum isolate 1432 small subunit ribosomal RNA
gene, partial sequence.
ACCESSION
AY268582
VERSION
AY268582.1 GI:33347884
KEYWORDS
Cryptosporidium parvum
SOURCE
Cryptosporidium parvum
ORGANISM
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
REFERENCE
1 (bases 1 to 744)
Xiao,L., Ryan,U.M., Graczyk,T.K., Limor,J., Li,L., Kombert,M.,
Junge,R., Sulaiman,I.M., Zhou,L., Arrowood,M.J., Koudela,B.,
Modry,D. and Lal,A.A.
Genetic diversity of Cryptosporidium spp. in captive reptiles
Appl. Environ. Microbiol. 70 (2), 891-899 (2004)
JOURNAL
PUBMED
14766569
REFERENCE
2 (bases 1 to 744)
Xiao,L.
Direct Submission
TITLE
Submitted (07-APR-2003) CDC, DPD/NCID, 4770 Buford Hwy, Atlanta, GA
JOURNAL

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30341, USA
Location/Qualifiers
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rRNA

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Db 23 CCGTAAAGTTATTATGAGTCACC 1

RESULT 15
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LOCUS
DEFINITION
Cryptosporidium parvum isolate 1444 small subunit ribosomal RNA
gene, partial sequence.
ACCESSION
AY268583
VERSION
AY268583.1 GI:33347885
KEYWORDS
Cryptosporidium parvum
SOURCE
Cryptosporidium parvum
ORGANISM
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
REFERENCE
1 (bases 1 to 748)
Xiao,L., Ryan,U.M., Graczyk,T.K., Limor,J., Li,L., Kombert,M.,
Junge,R., Sulaiman,I.M., Zhou,L., Arrowood,M.J., Koudela,B.,
Modry,D. and Lal,A.A.
Genetic diversity of Cryptosporidium spp. in captive reptiles
Appl. Environ. Microbiol. 70 (2), 891-899 (2004)
JOURNAL
PUBMED
14766569
REFERENCE
2 (bases 1 to 748)
Xiao,L.
Direct Submission
TITLE
Submitted (07-APR-2003) CDC, DPD/NCID, 4770 Buford Hwy, Atlanta, GA
JOURNAL
30341, USA
Location/Qualifiers
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rRNA

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Db 23 CCGTAAAGTTATTATGAGTCACC 1

Search completed: January 9, 2006, 19:54:14
Job time : 2257 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 16:34:41 ; Search time 327 Seconds
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Title: US-09-954-586-59

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Gapop 10.0 , Gapext 1.0

Searched: 4996997 seqs, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: Geneseqn2004bs:*
14: Geneseqn2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 1	23	100.0	23	6 AAD38427	Aad38427 Cryptospor
C 2	23	100.0	23	6 AAD38439	Aad38439 Cryptospor
C 3	23	100.0	23	6 AAD38445	Aad38445 Cryptospor
C 4	23	100.0	23	6 AAD38433	Aad38433 Cryptospor
C 5	23	100.0	1750	3 AAT90818	Aat90818 C. parvum
C 6	23	100.0	1750	3 AAA46368	Aaa46368 Nucleotid
C 7	18.8	81.7	447	2 Aaq71867	Aaq71867 G. vesicu
C 8	18.8	81.7	447	2 Aaq71870	Aaq71870 E. pisifo
C 9	18.8	81.7	447	2 Aaq71868	Aaq71868 G. intrar
C 10	18.8	81.7	512	8 ABZ56146	Abz56146 Aspergill
C 11	18.8	81.7	568	3 AAF11545	Aaf11545 Aspergill
C 12	18.8	81.7	568	13 ADU55586	Adu55586 Aspergill
C 13	18.8	81.7	568	14 ADZ93589	Adz93589 Aspergill
C 14	18.8	81.7	1024	3 AAF11316	Aaf11316 Aspergill
C 15	18.8	81.7	1024	13 ADU55357	Adu55357 Aspergill
C 16	18.8	81.7	1024	14 ADZ93360	Adz93360 Aspergill
C 17	18.8	81.7	1228	10 ABZ80030	Abz80030 Xylariale
C 18	18.8	81.7	1731	4 AAI68286	Aai68286 Bulgaria
C 19	18.8	81.7	1731	13 ADP79725	Adp79725 Anti-tumo

C 20	18.8	81.7	1733	2 AAZ00859	Aaz00859 A. fumiga
C 21	18.8	81.7	1733	13 ADP79724	Adp79724 Anti-tumo
C 22	18.8	81.7	2055	8 ABZ20766	Abz20766 Muscodor
C 23	18.8	81.7	2055	14 ADW86676	Adw86676 Muscodor
C 24	18.8	81.7	2089	8 ABZ20764	Abz20764 Muscodor
C 25	18.8	81.7	2089	14 ADW86674	Adw86674 Muscodor
C 26	18.2	79.1	433	12 ADN38639	Adn38639 DNA fragm
C 27	18.2	79.1	709	2 ADR01589	Adr01589 A. gossyp
C 28	17.8	77.4	1102	12 ADO10084	Ado10084 Novel hum
C 29	17.8	77.4	1102	6 ABQ93901	Abq93901 Human pro
C 30	17.8	77.4	1102	6 ABQ93902	Abq93902 Human pro
C 31	17.8	77.4	1102	2 ADO10082	Ado10082 Novel hum
C 32	17.2	74.8	444	2 AAQ71869	Aaq71869 G. margar
C 33	17.2	74.8	703	2 ADR01486	Adr01486 A. gossyp
C 34	17.2	74.8	723	2 ADR02260	Adr02260 A. gossyp
C 35	17.2	74.8	1732	12 ADH43081	Adh43081 18s rRNA
C 36	17.2	74.8	1734	5 ABK49559	Abk49559 Putrefact
C 37	17.2	74.8	1737	8 AAL51417	Aal51417 Spongipel
C 38	17.2	74.8	1740	11 ADZ11851	Adz11851 Candida a
C 39	17.2	74.8	1743	11 ADZ11854	Adz11854 Geotrichu
C 40	17.2	74.8	1764	14 ADV14619	Adv14619 Isbatichen
C 41	17.2	74.8	1776	4 AAF25849	Aaf25849 S. exiguu
C 42	17.2	74.8	1793	2 AAV60107	Aav60107 Rhizocton
C 43	17.2	74.8	1798	4 AAD14297	Aad14297 Yeast DNA
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C 45	17.2	74.8	1798	13 ADR32081	Adr32081 Genomic r

ALIGNMENTS

RESULT 1
AAD38427/c
ID AAD38427 standard; DNA; 23 BP.
XX
AC AAD38427;
XX
DT 10-SEP-2002 (first entry)
XX
DE Cryptosporidium sp. target DNA #9.
XX
KW Hybridisation; amplification; detection; da.
XX
OS Cryptosporidium sp.
XX
PN WO200222890-A2.
XX
PD 21-MAR-2002.
XX
PF 11-SEP-2001; 2001WO-US042192.
XX
PR 12-SEP-2000; 2000US-0232028P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Cunningham MM, Stull PD, Weisburg WG;
XX
DR WPI; 2002-454395/48.
XX
PT Novel oligonucleotides functioning as hybridization probes, helper probes and/or primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms, useful for detecting the organism in a test sample.
XX
PS Claim 23; Page 8; 133pp; English.
XX
CC The invention relates to oligonucleotides functioning as hybridisation assay probes, helper probes and/or amplification primers, targeted to nucleic acid sequences derived from Cryptosporidium organisms. Probes and primers of the invention are useful for detecting the presence of Cryptosporidium organisms in general and C. parvum organisms in particular in a test sample. The present sequence is Cryptosporidium sp. target DNA

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XX Best Local Similarity 100.0%; Pred. No. 0.56;
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DB 23 CCGTAAAGTTATTATGAGTCACC 1

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XX AAD38439;
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XX DT 10-SEP-2002 (first entry)
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XX Cryptosporidium sp. target DNA #15.
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XX Hybridisation; amplification; detection; ds.
XX
XX Cryptosporidium sp.
XX
XX WO200222890-A2.
XX
XX 21-MAR-2002.
XX
XX 11-SEP-2001; 2001WO-US042192.
XX
XX 12-SEP-2000; 2000US-0232028P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Cunningham MM, Stull PD, Weisburg WG;
XX
XX WPI; 2002-454395/48.
XX
XX Novel oligonucleotides functioning as hybridization probes, helper probes
XX and/or primers, targeted to nucleic acid sequences derived from
XX Cryptosporidium organisms, useful for detecting the organism in a test
XX sample.
XX
XX Claim 23; Page 8; 133pp; English.
XX
XX The invention relates to oligonucleotides functioning as hybridisation
XX assay probes, helper probes and/or amplification primers, targeted to
XX nucleic acid sequences derived from Cryptosporidium organisms. Probes and
XX primers of the invention are useful for detecting the presence of
XX Cryptosporidium organisms in general and C. parvum organisms in
XX particular in a test sample. The present sequence is Cryptosporidium sp.
XX target DNA
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XX WPI; 2002-454395/48.
XX
XX Novel oligonucleotides functioning as hybridization probes, helper probes
XX and/or primers, targeted to nucleic acid sequences derived from
XX Cryptosporidium organisms, useful for detecting the organism in a test
XX sample.
XX
XX Claim 23; Page 8; 133pp; English.
XX
XX The invention relates to oligonucleotides functioning as hybridisation
XX assay probes, helper probes and/or amplification primers, targeted to
XX nucleic acid sequences derived from Cryptosporidium organisms. Probes and
XX primers of the invention are useful for detecting the presence of
XX Cryptosporidium organisms in general and C. parvum organisms in
XX particular in a test sample. The present sequence is Cryptosporidium sp.
XX target DNA
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XX Best Local Similarity 100.0%; Pred. No. 0.56;
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XX DT 10-SEP-2002 (first entry)
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XX Hybridisation; amplification; detection; ss.
XX
XX Cryptosporidium sp.
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XX WO200222890-A2.
XX
XX 21-MAR-2002.
XX
XX 11-SEP-2001; 2001WO-US042192.
XX
XX 12-SEP-2000; 2000US-0232028P.
XX
XX (GENP-) GEN-PROBE INC.
XX
XX Cunningham MM, Stull PD, Weisburg WG;
XX
XX WPI; 2002-454395/48.
XX
XX Novel oligonucleotides functioning as hybridization probes, helper probes
XX and/or primers, targeted to nucleic acid sequences derived from
XX Cryptosporidium organisms, useful for detecting the organism in a test
XX sample.
XX
XX Claim 23; Page 8; 133pp; English.
XX
XX The invention relates to oligonucleotides functioning as hybridisation
XX assay probes, helper probes and/or amplification primers, targeted to
XX nucleic acid sequences derived from Cryptosporidium organisms. Probes and
XX primers of the invention are useful for detecting the presence of
XX Cryptosporidium organisms in general and C. parvum organisms in
XX particular in a test sample. The present sequence is Cryptosporidium sp.
XX target RNA
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XX Sequence 23 BP; 7 A; 5 C; 4 G; 0 T; 7 U; 0 Other;
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XX Query Match 100.0%; Score 23; DB 6; Length 23;
XX Best Local Similarity 69.6%; Pred. No. 0.56;
XX Matches 16; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
DB 1 CCGTAAAGUUUUAUGAGUCACC 23

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ID AAD38433 standard; RNA; 23 BP.
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XX AAD38433;
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XX 10-SEP-2002 (first entry)
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XX Cryptosporidium sp. target RNA #9.
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XX Hybridisation; amplification; detection; ss.
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XX Cryptosporidium sp.
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XX WO200222890-A2.
XX
XX 21-MAR-2002.
XX
XX 11-SEP-2001; 2001WO-US042192.
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XX 12-SEP-2000; 2000US-0232028P.
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XX (GENP-) GEN-PROBE INC.
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XX Cunningham MM, Stull PD, Weisburg WG;
XX
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DR WPI; 2002-454395/48.
 XX Novel oligonucleotides functioning as hybridization probes, helper probes
 PT and/or primers, targeted to nucleic acid sequences derived from
 PT Cryptosporidium organisms, useful for detecting the organism in a test
 PT sample.
 XX
 PS Claim 23; Page 8; 133pp; English.
 XX
 CC The invention relates to oligonucleotides functioning as hybridisation
 CC assay probes, helper probes and/or amplification primers, targeted to
 CC nucleic acid sequences derived from Cryptosporidium organisms. Probes and
 CC primers of the invention are useful for detecting the presence of
 CC Cryptosporidium organisms in general and C. parvum organisms in
 CC particular in a test sample. The present sequence is Cryptosporidium sp.
 CC target RNA
 XX
 SQ Sequence 23 BP; 7 A; 4 C; 5 G; 0 T; 7 U; 0 Other;
 Query Match 100.0%; Score 23; DB 6; Length 23;
 Best Local Similarity 100.0%; Pred. No. 0.56; Length 23;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGTAAAGTTATTATGAGTCACC 23
 |||||
 DB 23 CCGTAAAGTTATTATGAGTCACC 1
 RESULT 5
 AAT90818/c
 ID AAT90818 standard; DNA; 1750 BP.
 XX
 AC AAT90818;
 XX
 DT 22-APR-1998 (first entry)
 XX
 DE C. parvum 18S rRNA gene.
 XX
 KW PCR primer; amplify; C. parvum; 18S rRNA gene; forensic analysis;
 KW microorganism classification; target nucleic acid sequence segregation;
 KW genetic abnormality identification; inborn error of metabolism;
 KW infectious disease diagnosis; ss.
 XX
 OS Cryptosporidium parvum.
 XX
 FN WO9735026-A1.
 XX
 PD 25-SEP-1997.
 XX
 PF 17-MAR-1997; 97WO-US004170.
 XX
 PR 18-MAR-1996; 96US-00617045.
 XX
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.
 XX
 PI Wick JF, Mueller R, Blasak ML, Wilkosz RK;
 XX
 DR WPI; 1997-480231/44.
 XX
 PT Segregating copy of target nucleic acid sequence found in single stranded
 PT polynucleotide - by serial generation of double stranded DNA containing
 PT extended terminal nicking sites, to displace any existing
 PT polynucleotide(s).
 XX
 PS Disclosure; Page 60-62; 92pp; English.
 XX
 CC This sequence represents the C. parvum 18S rRNA gene which can be
 CC isolated using the sequences represented by AAT90815-T90817 in the method
 CC of the invention. The method is for segregating a copy of a target
 CC nucleic acid sequence (I) found in a single stranded polynucleotide (II),
 CC which is suitable for use in amplifying (I). The methods for the
 CC amplification, detection and quantification of specific (I) can be used
 CC in microorganism classification, identification of genetic abnormalities

CC including inborn errors of metabolism, diagnosis of infectious diseases,
 CC forensic analysis, environmental testing and studies involving
 CC developmental and cellular biology. The methods are versatile, reliable
 CC and simple and are capable of amplifying both RNA and DNA, and should do
 CC so exponentially, using a minimum number of primers under substantially
 CC isostatic conditions
 XX
 SQ Sequence 1750 BP; 533 A; 292 C; 390 G; 535 T; 0 U; 0 Other;
 Query Match 100.0%; Score 23; DB 2; Length 1750;
 Best Local Similarity 100.0%; Pred. No. 0.65; Length 1750;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGTAAAGTTATTATGAGTCACC 23
 |||||
 DB 254 CCGTAAAGTTATTATGAGTCACC 232
 RESULT 6
 AAA46368/c
 ID AAA46368 standard; DNA; 1750 BP.
 XX
 AC AAA46368;
 XX
 DT 04-SEP-2000 (first entry)
 XX
 DE Nucleotide sequence of the 18S ribosomal DNA of C. parvum.
 XX
 KW Isothermal amplification; hemi-modified restriction endonuclease;
 KW restriction endonuclease; 18S ribosomal DNA; ss.
 XX
 OS Cryptosporidium parvum.
 XX
 FN WC200028084-A1.
 XX
 PD 18-MAY-2000.
 XX
 PF 05-NOV-1999; 99WO-US025927.
 XX
 PR 06-NOV-1998; 98US-00186910.
 XX
 PA (MOLE-) MOLECULAR BIOLOGY RESOURCES INC.
 XX
 PI Jolly JF;
 XX
 DR WPI; 2000-376589/32.
 XX
 PT Isothermal method for amplifying a target nucleic acid, with improved
 PT thermodynamics and kinetics over prior art methods.
 XX
 PS Example 1; Page 47-49; 64pp; English.
 XX
 CC The specification describes an isothermal target nucleic acid
 CC amplification method. The method comprises contacting a mixture of a
 CC target, two primers containing hemi-modified restriction endonuclease
 CC sites and modified nucleotides capable of forming phosphodiester bonds,
 CC and a polymerase lacking 5' to 3' exonuclease activity, with a
 CC restriction endonuclease, and incubating under isothermal conditions. The
 CC method can be used for amplifying nucleotide sequences. The method
 CC exhibits improved thermodynamics and kinetics, resulting in increased
 CC sensitivity and polynucleotide length, thus broadening both the range of
 CC target sources and the range of target lengths. The present sequence
 CC represents the 18S ribosomal DNA of C. parvum, and contains a RNA target
 CC (nucleotides 937-1095) which is used to demonstrate the method of the
 CC invention
 XX
 SQ Sequence 1750 BP; 533 A; 292 C; 390 G; 535 T; 0 U; 0 Other;
 Query Match 100.0%; Score 23; DB 3; Length 1750;
 Best Local Similarity 100.0%; Pred. No. 0.65; Length 1750;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CCGTAAAGTTATTATGAGTCACC 23

Db 254 CCGTAAAGTTATTATGAGTCACC 232
|||||

RESULT 7
AAQ71867/c

ID AAQ71867 standard; DNA; 447 BP.

XX AC AAQ71867;

XX DT 23-MAR-1995 (first entry)

XX DE G. vesiculiferum small ribosomal subunit RNA.

XX KW Nuclear 18S ribosomal gene; SSU; probe; primer;

XX KW arbuscular endomycorrhizal fungi; plant; root; ds.

XX OS Glomus vesiculiferum.

XX PN CA2086136-A.

XX PD 24-JUN-1994.

XX PF 23-DEC-1992; 92CA-02086136.

XX PR 23-DEC-1992; 92CA-02086136.

XX PA (SIMO/) SIMON L.

XX PI Simon L, Lalonde M;

XX DR WPI; 1994-264577/33.

XX PT New oligonucleotide probes - used for the detection of arbuscular
endomycorrhizal fungi in plant root samples.

XX PS Disclosure; Page 18; 40pp; English.

XX CC The gene sequence of the small ribosomal subunit RNA of arbuscular
endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
intraradices and Gigaspora margarita were compared with that of a non-
arbuscular endomycorrhizal fungus, Endogone pisiformis, in order to
design taxon specific primers/probes

XX SQ Sequence 447 BP; 135 A; 86 C; 107 G; 118 T; 0 U; 1 Other;

Query Match 81.7%; Score 18.8; DB 2; Length 447;

Best Local Similarity 90.9%; Pred. No. 57;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGTAAAGTTATTATGAGTCACC 23

Db 158 CGAAAGTTATTATGAATCACC 137
|||

RESULT 8

AAQ71870/c

ID AAQ71870 standard; DNA; 447 BP.

XX AC AAQ71870;

XX DT 23-MAR-1995 (first entry)

XX DE E. pisiformis small ribosomal subunit RNA.

XX KW Nuclear 18S ribosomal gene; SSU; probe; primer;

XX KW arbuscular endomycorrhizal fungi; plant; root; ds.

XX OS Endogone pisiformis.

XX FH Key Location/Qualifiers

FT misc_difference 116..135

FT /*tag= a

/note= "bases not determined"

XX PN CA2086136-A.

XX PD 24-JUN-1994.

XX PF 23-DEC-1992; 92CA-02086136.

XX PR 23-DEC-1992; 92CA-02086136.

XX PA (SIMO/) SIMON L.

XX PI Simon L, Lalonde M;

XX DR WPI; 1994-264577/33.

XX PT New oligonucleotide probes - used for the detection of arbuscular
endomycorrhizal fungi in plant root samples.

XX PS Disclosure; Page 20; 40pp; English.

XX CC The gene sequence of the small ribosomal subunit RNA of arbuscular
endomycorrhizal fungi obtained from Glomus vesiculiferum, Glomus
intraradices and Gigaspora margarita were compared with that of a non-
arbuscular endomycorrhizal fungus, Endogone pisiformis, in order to
design taxon specific primers/probes

XX SQ Sequence 447 BP; 133 A; 77 C; 100 G; 117 T; 0 U; 20 Other;

Query Match 81.7%; Score 18.8; DB 2; Length 447;

Best Local Similarity 90.9%; Pred. No. 57;

Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGTAAAGTTATTATGAGTCACC 23

Db 158 CGAAAGTTATTATGAATCACC 137
|||

RESULT 9

AAQ71868/c

ID AAQ71868 standard; DNA; 447 BP.

XX AC AAQ71868;

XX DT 23-MAR-1995 (first entry)

XX DE G. intraradices small ribosomal subunit RNA.

XX KW Nuclear 18S ribosomal gene; SSU; probe; primer;

XX KW arbuscular endomycorrhizal fungi; plant; root; ds.

XX OS Glomus intraradices.

XX PN CA2086136-A.

XX PD 24-JUN-1994.

XX PF 23-DEC-1992; 92CA-02086136.

XX PR 23-DEC-1992; 92CA-02086136.

XX PA (SIMO/) SIMON L.

XX PI Simon L, Lalonde M;

XX DR WPI; 1994-264577/33.

XX PT New oligonucleotide probes - used for the detection of arbuscular
endomycorrhizal fungi in plant root samples.

XX PS Disclosure; Page 19; 40pp; English.

XX CC The gene sequence of the small ribosomal subunit RNA of arbuscular

CC endomycorrhizal fungi obtained from *Glomus vesiculiferum*, *Glomus*
CC intraradices and *Gigaspora margarita* were compared with that of a non-
CC arbuscular endomycorrhizal fungus, *Endogone pisiformis*, in order to
CC design taxon specific primers/probes

XX
SQ Sequence 447 BP; 137 A; 86 C; 107 G; 117 T; 0 U; 0 Other;
Query Match 81.7%; Score 18.8; DB 2; Length 447;
Best Local Similarity 90.9%; Pred. No. 57;
Matches 20: Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23
|||
Db 158 CGAAAAGTTATTATGAATCACC 137

RESULT 10
ABZ56146/c
ID ABZ56146 standard: CDNA: 512 BP.

XX
 SQ Sequence 512 BP; 150 A; 105 C; 123 G; 134 T; 0 U; 0 Other;

 Query Match 81.7%; Score 18.8; DB 8; Length 512;
 Best Local Similarity 90.9%; Pred. No. 57;
 Matches 20. Conservative 0; Mismatches 2; Indels 0; Gaps 0;

2 CGTAAAGTTATTAGATCACC 23

db 227 CGTTAAGTTATTATGAATCACC 206

RESULT 11
AAFL1545/c
ID AAF11545 standard; cDNA; 568 BP.
XX
XX AC AAF11545;
XX AC
XX
DT 13-MAR-2001 (first entry)
XX
XX
DE Aspergillus niger EST SEO ID NO:4068.

Sequence 568 BP: 155 A; 116 C; 141 G; 150 T; 0 U; 6 Other;

Query Match	81.7%	Score 18.8;	DB 3;	Length 568;
Best Local Similarity	90.9%;	Pred. No. 58;		
Matches 20:	Conservative	0;	Mismatches	2;
	Indels	0;	Gaps	0;

QY 2 CGTAAAGTTATTATGAGTCACC 23
Best Local Similarity 90.9%; Pred. No. 58; Length 568;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 249 CGTTAAGTTATTATGAGTCACC 228

RESULT 12
ADU55586/C
ID ADU55586 standard; cDNA; 568 BP.
XX AC ADU55586;
XX 10-FEB-2005 (first entry)
XX Aspergillus niger strain Bo-95 EST, SEQ ID NO:4068.
DE Gene expression; biochip; microarray; hybridization; EST;
KW expressed sequence tag; ss.
XX Aspergillus niger; strain Bo-95.
OS US2004229367-A1.
PN 18-NOV-2004.
XX 29-AUG-2003; 2003US-00653047.
XX 22-MAR-1999; 99US-00273623.
PR 22-MAR-2000; 2000US-00533559.
XX (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES INC AS.
XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
PI WPI; 2004-832481/82.
XX Monitoring differential expression of genes in a filamentous fungal cell
PT relative to expression of the genes in second filamentous fungal cells,
PT comprises using microarrays containing Fusarium venenatum expressed
PT sequence tags.
XX Example 11; SEQ ID NO 4068; 274pp; English.
XX The invention relates to a method for monitoring the differential
CC expression of genes in a first filamentous fungal cell relative to the
CC same genes in one or more second filamentous fungal cells. The method
CC involves differentially labeling nucleic acids from the first and second
CC fungal cells with fluorescent reporter dyes, and adding the mixture of
CC fluorescently labeled polynucleotides to a substrate containing an array
CC of Fusarium venenatum expressed sequence tags (ESTs) selected from
CC ADU51519-ADU5288 under conditions that permit hybridization. Relative
CC expression of genes in the fungal cells is determined by fluorescence;
CC the fluorescent signal emitted when labeled nucleic acids from the first
CC fungal cell bind to the ESTs in the array differs in color from that
CC emitted when labeled nucleic acids from the second fungal cell hybridize.
CC When both sets of labeled nucleic acids bind to the array, a distinct
CC combined fluorescence emission color is produced. The filamentous fungal
CC cells used in the method are chosen from Acremonium, Aspergillus,
CC Fusarium, Humicola, Mucor, Myceliophthora, Neurospora, Penicillium,
CC Thielavia, Tolypocladium, and Trichoderma cells, preferably Fusarium
CC venenatum, Aspergillus niger, or Aspergillus oryzae. The method of the
CC invention is useful for monitoring the expression of a plurality of genes
CC in filamentous fungal cells, in order to improve the cells' protein
CC production capacity when such organisms are used for the industrial
CC production of proteins (e.g., enzymes). Sequences ADU5289-ADU55894
CC represent ESTs derived from Aspergillus niger strain Bo-95 which were
CC obtained in an example of the invention. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from the US patent office at
CC seqdata.uspto.gov/sequence.html?DocID=US20040222367.
XX Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 0 U; 6 Other;

Query Match 81.7%; Score 18.8; DB 13; Length 568;
Best Local Similarity 90.9%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23
Best Local Similarity 90.9%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 249 CGTTAAGTTATTATGAGTCACC 228

RESULT 13
ADZ93589/C
ID ADZ93589 standard; cDNA; 568 BP.
XX AC ADZ93589;
XX 11-AUG-2005 (first entry)
XX Aspergillus niger expressed sequence tag cDNA SEQ ID NO 4068.
DE differential expression; gene expression; filamentous fungus;
KW expressed sequence tag; EST; variation; microarray; ss.
XX Aspergillus niger.
OS US6902887-B1.
PN 07-JUN-2005.
XX 22-MAR-2000; 2000US-00533559.
PR 22-MAR-1999; 99US-00273623.
XX (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES AS.
XX Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
PI WPI; 2005-401635/41.
XX Monitoring differential expression of genes in first filamentous fungal
PT cell relative to that of genes in second fungal cells, comprises
PT hybridizing fluorescence labeled nucleic acids from the cells to an array
PT of expressed sequence tags.
XX Disclosure; SEQ ID NO 4068; 264pp; English.
XX The invention relates to a method of monitoring (M1) differential
CC expression of multiple genes in a first filamentous fungal cell relative
CC to expression of the same genes in one or more second filamentous fungal
CC cells, comprises adding fluorescence labeled nucleic acids isolated from
CC the cells to a substrate containing an array of Aspergillus oryzae
CC expressed sequence tag (EST) of ADZ93898-ADZ96922, and examining the
CC array under fluorescence excitation conditions. (M1) is useful for
CC monitoring global expression of several genes from a filamentous fungal
CC cell, discovering new genes, identifying possible functions of unknown
CC open reading frames and monitoring gene copy number variation and
CC stability. In (M1), one spot on an array equals one gene or open reading
CC frame, extensive follow-up characterization is unnecessary since sequence
CC information is available and EST microarrays can be organized based on
CC function of the gene products. This sequence corresponds to an EST
CC sequence of the invention. (Note: this sequence is not given in the
CC printed specification but can be obtained in electronic form from the
CC USPTO web site seqdata.uspto.gov/sequence.html; Document ID: 6902887B1).
XX Sequence 568 BP; 155 A; 116 C; 141 G; 150 T; 0 U; 6 Other;

Query Match 81.7%; Score 18.8; DB 14; Length 568;
Best Local Similarity 90.9%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23
Best Local Similarity 90.9%; Pred. No. 58;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGATCACC 23
DB 57 CGTTAAGTTATTATGATCACC 36

RESULT 15
ADU55357/c
ID ADU55357 standard; cDNA; 1024 BP.
AC ADU55357;
XX
DT 10-FEB-2005 (first entry)
XX
DE Aspergillus niger strain Bo-95 EST, SEQ ID NO:3839.
XX
KW Gene expression; biochip; microarray; hybridization; EST;
KW expressed sequence tag; ss.
XX
OS Aspergillus niger; strain Bo-95.
XX
PN US2004223367-A1.
XX
PD 18-NOV-2004.
XX
PF 29-AUG-2003; 2003US-00653047.
XX
PR 22-MAR-1999; 99US-00273623.
PR 22-MAR-2000; 2000US-00533559.
XX
PA (NOVO) NOVOZYMES BIOTECH INC.
PA (NOVO) NOVOZYMES INC AS.
XX
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX
DR WPI; 2004-832481/82.
XX
PT Monitoring differential expression of genes in a filamentous fungal cell
PT relative to expression of the genes in second filamentous fungal cells,
PT comprises using microarrays containing Fusarium venenatum expressed
PT sequence tags.
XX
PS Example 11; SEQ ID NO 3839; 274pp; English.
XX

The invention relates to a method for monitoring the differential expression of genes in a first filamentous fungal cell relative to the same genes in one or more second filamentous fungal cells. The method involves differentially labeling nucleic acids from the first and second fungal cells with fluorescent reporter dyes, and adding the mixture of fluorescently labeled polynucleotides to a substrate containing an array of Fusarium venenatum expressed sequence tags (ESTs) selected from ADU51519-ADU55288 under conditions that permit hybridization. Relative expression of genes in the fungal cells is determined by fluorescence; the fluorescent signal emitted when labeled nucleic acids from the first fungal cell bind to the ESTs in the array differs in color from that emitted when labeled nucleic acids from the second fungal cell hybridise. When both sets of labeled nucleic acids bind to the array, a distinct combined fluorescence emission color is produced. The filamentous fungal cells used in the method are chosen from Acremonium, Aspergillus, Fusarium, Humicola, Mucor, Mycelophthora, Neurospora, Penicillium, Thielavia, Tolypocladium, and Trichoderma cells, preferably Fusarium venenatum, Aspergillus niger, or Aspergillus oryzae. The method of the invention is useful for monitoring the expression of a plurality of genes in filamentous fungal cells, in order to improve the cells' protein production capacity when such organisms are used for the industrial production of proteins (e.g., enzymes). Sequences ADU55289-ADU55894 represent ESTs derived from Aspergillus niger strain Bo-95 which were obtained in an example of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the US patent office at seqdata.uspto.gov/sequence.html?docID=US20040222367.

Sequence 1024 BP; 275 A; 204 C; 275 G; 269 T; 0 U; 1 Other;

DB 249 CGTTAAGTTATTATGATCACC 228

RESULT 14
AAF11316/c
ID AAF11316 standard; cDNA; 1024 BP.
AC AAF11316;
XX
DT 13-MAR-2001 (first entry)
XX
DE Aspergillus niger EST SEQ ID NO:3839.
XX
KW Multiple gene expression; filamentous fungal cell; EST;
KW expressed sequence tag; Fusarium venenatum; Aspergillus niger;
KW Aspergillus oryzae; Trichoderma reesei; identification; recombination;
KW culture condition; environmental stress; spore morphogenesis;
KW metabolic pathway engineering; catabolic pathway engineering; ss.
XX
OS Aspergillus niger.
XX
PN WO200056762-A2.
XX
PD 28-SEP-2000.
XX
PF 22-MAR-2000; 2000WO-US007781.
XX
PR 22-MAR-1999; 99US-00273623.
XX
PA (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO NORDISK AS.
XX
PI Berka RM, Rey MW, Shuster JR, Kauppinen S, Clausen IG, Olsen PB;
XX
DR WPI; 2000-594572/56.
XX
PT Monitoring differential expression of genes in filamentous fungal cells
PT uses fluorescence-labeled nucleic acids isolated from the cells and a
PT substrate of expressed sequence tags.
XX
PS Claim 87; Page 1718; 3161pp; English.
XX

The present invention describes a method for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. The method uses fluorescence-labeled nucleic acids isolated from the FF cells and a substrate of expressed sequence tags (EST). The ESTs are used in the methods for monitoring differential expression of genes in a first filamentous fungal (FF) cell relative to expression of the same genes in one or more second filamentous fungal cells. Monitoring the global expression of genes from FF cells allows the production potential of the microorganisms to be improved. New genes may be discovered, possible functions of unknown open reading frames can be identified and gene copy number variation and stability can be monitored. The expression of genes can be used to study how FF cells adapt to changes in culture conditions, environmental stress, spore morphogenesis, recombination, metabolic or catabolic pathway engineering. Using ESTs provides several advantages over genomic or random cDNA clones including elimination of redundancy as one spot on an array equals one gene or open reading frame, and organisation of the microarrays based on function of the gene products to facilitate analysis of the results. AAF07478 to AAF11247 represents ESTs from Fusarium venenatum; AAF11248 to AAF11853 represents ESTs from Aspergillus niger; AAF11854 to AAF14878 represents ESTs from Aspergillus oryzae; and AAF14879 to AAF15337 represents ESTs from Trichoderma reesei, which are all specifically claimed in the present invention

Sequence 1024 BP; 275 A; 204 C; 275 G; 269 T; 0 U; 1 Other;

Query Match 81.7%; Score 18.8; DB 3; Length 1024;
Best Local Similarity 90.9%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Query Match 81.7%; Score 18.8; DB 13; Length 1024;
Best Local Similarity 90.9%; Pred. No. 59;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23
||| ||||| ||||| ||||| |||||
Db 57 CGTTAAGTTATTATGAGTCACC 36

Search completed: January 9, 2006, 18:38:56
Job time : 329 secs

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 18:15:11 ; Search time 2474 Seconds
(without alignments)
434.965 Million cell updates/sec

Title: US-09-954-586-59
Perfect score: 23
Sequence: 1 ccgtaagtattatgagtcacc 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hcc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_gss1.*
10: gb_gss2.*
11: gb_gss3.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	23	100.0	254	1 AA532319	AA532319 CpEST.449
C 2	23	100.0	427	1 AA167899	AA167899 CpEST.044
C 3	23	100.0	461	1 AA167914	AA167914 CpEST.013
C 4	23	100.0	485	1 AA167900	AA167900 CpEST.045
C 5	23	100.0	520	1 AA167911	AA167911 CpEST.003
C 6	23	100.0	566	1 AA167858	AA167858 CpEST.052
C 7	23	100.0	737	9 A0935911	A0935911 CpG27168
C 8	23	100.0	759	1 AJ797385	AJ797385 AJ797385
C 9	23	100.0	770	9 A0254527	A0254527 CpG06798
C 10	21	91.3	593	11 CPA563207	AJ563207 Cryptospor
C 11	20.4	88.7	539	6 CA685830	CA685830 wlm36.pko
C 12	20.4	88.7	907	1 AU066519	AU066519 TAS007.B0
C 13	19.8	86.1	558	2 BE430105	BE430105 TAS007.B0
C 14	19.8	86.1	769	8 DR045104	DR045104 FP-7 G03.
C 15	19.8	86.1	771	8 DN476855	DN476855 alt212xe
C 16	19.8	86.1	895	8 DN475823	DN475823 alt201xm
C 17	19.8	86.1	1110	8 DR044870	DR044870 FP-5 C09.
C 18	19.4	84.3	518	3 BM959056	BM959056 PLATE12
C 19	19.4	84.3	520	1 AU014209	AU014209 AU014209
C 20	19.4	84.3	531	1 AU010089	AU010089 AU010089
C 21	18.8	81.7	122	1 AA783903	AA783903 c8h04a1.f
C 22	18.8	81.7	195	7 CO149687	CO149687 EST824740

C 23	18.8	81.7	196	7 CO151388	CO151388 EST826441
C 24	18.8	81.7	244	1 AI212196	AI212196 w9f07a1.f
C 25	18.8	81.7	246	6 CD148090	CD148090 ML1-0008T
C 26	18.8	81.7	250	1 AA784878	AA784878 g3a04a1.f
C 27	18.8	81.7	252	1 AI211979	AI211979 v7h05a1.f
C 28	18.8	81.7	263	7 CO147914	CO147914 EST822967
C 29	18.8	81.7	268	1 AA783154	AA783154 C1f02a1.f
C 30	18.8	81.7	269	1 AA966666	AA966666 w7f12a1.f
C 31	18.8	81.7	271	7 CO137477	CO137477 EST832148
C 32	18.8	81.7	273	1 AA966294	AA966294 v7h05a1.f
C 33	18.8	81.7	278	7 CV191588	CV191588 1.O11 SSH
C 34	18.8	81.7	280	1 AA965352	AA965352 e3g08a1.f
C 35	18.8	81.7	293	1 AA783904	AA783904 c8h04a1.f
C 36	18.8	81.7	295	1 AA788074	AA788074 r4f04a1.f
C 37	18.8	81.7	295	1 AI327731	AI327731 10c01a1.f
C 38	18.8	81.7	303	7 CO140200	CO140200 EST834871
C 39	18.8	81.7	304	7 CO136756	CO136756 EST831427
C 40	18.8	81.7	305	7 CO140190	CO140190 EST834861
C 41	18.8	81.7	308	1 AA785043	AA785043 g4e05a1.f
C 42	18.8	81.7	317	1 AA785195	AA785195 g5f07a1.f
C 43	18.8	81.7	320	7 CO152456	CO152456 EST827509
C 44	18.8	81.7	321	1 AA966439	AA966439 w5a05a1.f
C 45	18.8	81.7	329	1 AA965722	AA965722 o4e03a1.f

ALIGNMENTS

RESULT 1
AA532319/c
LOCUS CPES.449 unizAPCpIOWAsporolib3 Cryptosporidium parvum cDNA 5',
DEFINITION mRNA sequence.
ACCESSION AA532319 GI:2276511
VERSION AA532319.1
KEYWORDS EST.
SOURCE Cryptosporidium parvum
ORGANISM Cryptosporidium parvum
REFERENCE 1 (bases 1 to 254)
AUTHORS Strong, W.B. and Nelson, R.G.
TITLE Preliminary profile of the Cryptosporidium parvum genome: an
expressed sequence tag and genome survey sequence analysis
JOURNAL Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
PUBMED 10717299
COMMENT Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
Francisco
Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' to
the insert, to correct misallied bases and assign uncalled (N)
bases throughout the sequence, and to terminate when base-calling
became ambiguous.
Seq primer: M13 reverse
High quality sequence stop: 254.
Location/Qualifiers
1. .254
/organism="Cryptosporidium parvum"
/mol_type="mRNA"
/db_xref="taxon:5807"
/dev_stage="sporozoite"
/lab_host="E. coli XLI Blue MRF' Kan"
/clone_lib="unizAPCpIOWAsporolib3"
/note="Vector: UNIZAP XR; Site 1: EcoR I; Site 2: Xho I;
The C. parvum cDNA library was prepared by Drs. Norman J.
Pieniazek, Michael J. Arrowood, Susan B. Slemenda, and Jan
R. Mead at the Centers for Disease Control and Prevention

(Atlanta, Georgia). Poly A+ RNA was separated from total C. parvum RNA using the Poly(A) Quik mRNA Isolation Kit from Stratagene. Directional cDNA was synthesized by first-strand priming with a Xho I-oligo d(T) linker-primer, second-stranding with RNase H and DNA polymerase I, ligation of EcoR I linkers, and digestion with Xho I, all using the Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the unamplified library was >95% recombinant and contained 3.8 X 10(6) independent clones. PCR analysis of 20 random clones indicated that the average insert size was ca. 1.1 kb."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 254;
Best Local Similarity 100.0%; Pred. No. 2.7;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
|||||
Db 227 CCGTAAAGTTATTATGAGTCACC 205

RESULT 2

AA167899/c
LOCUS
DEFINITION
CpEST.044 unizAPcPIOWAsporolibi Cryptosporidium parvum cDNA 5' similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AA167899.1 GI:1746067
Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
1 (bases 1 to 427)
Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
10717299

Contact: Nelson, R. G.
Dep't. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San Francisco
Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu

Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.

Seq primer: M13 reverse
High quality sequence stop: 427.
Location/Qualifiers

FEATURES
source

1. .427
/organism="Cryptosporidium parvum"
/mol_type="mRNA"
/strain="IOWA"
/db_xref="taxon:5807"
/dev_stage="sporozoite"
/lab_host="E. coli XL1 Blue MRF' Kan"
/clone_lib="unizAPcPIOWAsporolibi"
/notes="Vector: UnizAP XR; Site 1: EcoR I; Site 2: Xho I;
Total RNA was isolated from purified Cryptosporidium parvum sporozoites using TRIzol reagent (GIBCO-BRL). Directional cDNA was synthesized by first-strand priming with a Xho I-oligo d(T) linker-primer, second-stranding with RNase H and DNA polymerase I, ligation of EcoR I linkers, and digestion with Xho I, all using the Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned

into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the primary library was >97% recombinant and contained 1.3 X 10(6) independent clones with an ca. average insert size of 1.3 kb. Based on open reading frame (orf) analysis of the first 64 sequence tags we estimate that up to one-third of the library is composed of genomic DNA clones since approximately 15% of the orfs were incorrectly oriented on the antisense strand."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 427;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
|||||
Db 235 CCGTAAAGTTATTATGAGTCACC 213

RESULT 3

AA167914/c
LOCUS
DEFINITION
AA167914 461 bp mRNA linear EST 23-AUG-2000
CpEST.013 unizAPcPIOWAsporolibi Cryptosporidium parvum cDNA 5' similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
AA167914.1 GI:1746082
Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
1 (bases 1 to 461)
Strong, W.B. and Nelson, R.G.
Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
10717299

Contact: Nelson, R. G.
Dep't. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San Francisco
Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu

Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.

Seq primer: M13 reverse
High quality sequence stop: 461.
Location/Qualifiers

FEATURES
source

1. .461
/organism="Cryptosporidium parvum"
/mol_type="mRNA"
/strain="IOWA"
/db_xref="taxon:5807"
/dev_stage="sporozoite"
/lab_host="E. coli XL1 Blue MRF' Kan"
/clone_lib="unizAPcPIOWAsporolibi"
/notes="Vector: UnizAP XR; Site 1: EcoR I; Site 2: Xho I;
Total RNA was isolated from purified Cryptosporidium parvum sporozoites using TRIzol reagent (GIBCO-BRL). Directional cDNA was synthesized by first-strand priming with a Xho I-oligo d(T) linker-primer, second-stranding with RNase H and DNA polymerase I, ligation of EcoR I linkers, and digestion with Xho I, all using the Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned into the EcoR I and Xho I sites of Lambda Uni-ZAP XR vector; the primary library was >97% recombinant and contained 1.3 X 10(6) independent clones with an ca. average insert size of 1.3 kb. Based on open reading frame

(orf) analysis of the first 64 sequence tags we estimate that up to one-third of the library is composed of genomic DNA clones since approximately 15% of the orfs were incorrectly oriented on the antisense strand."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 461;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTATGAGTCACC 23
|||||
Db 233 CCGTAAAGTTATTATGAGTCACC 211

RESULT 4

AA167900/c
LOCUS
DEFINITION
cPEST.045 unizAPCpIOWAsporLib1 Cryptosporidium parvum cDNA 5', similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA sequence.

ACCESSION

AA167900
VERSION
KEYWORDS
SOURCE

ORGANISM

Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Cryptosporidiidae; Cryptosporidium.

REFERENCE

1 (bases 1 to 485)

AUTHORS

Strong, W.B. and Nelson, R.G.

TITLE

Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis

JOURNAL

Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)

PUBMED

10717299

COMMENT

Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San Francisco
Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.

Seq primer: M13 reverse

High quality sequence stop: 485.

Location/Qualifiers

FEATURES

source

1. 485

/organism="Cryptosporidium parvum"

/mol_type="mRNA"

/strain="IOWA"

/db_xref="taxon:5807"

/dev_stage="sporozoite"

/lab_host="E. coli XL1 Blue MRF' Kan"

/clone_lib="unizAPCpIOWAsporLib1"

/note="Vector: UniZAP XR; Site_1: EcoR I; Site_2: Xho I;

Total RNA was isolated from purified Cryptosporidium

parvum sporozoites using TRIZOL reagent (GIBCO-BRL).

Directional cDNA was synthesized by first-strand priming

with a Xho I-oligo d(T) linker-primer, second-stranding

with RNase H and DNA polymerase I, ligation of EcoR I

linkers, and digestion with Xho I, all using the

Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned

into the EcoR I and Xho I sites of Lambda Uni-ZAP XR

vector; the primary library was >97% recombinant and

contained 1.3 X 10(6) independent clones with an ca.

average insert size of 1.3 kb. Based on open reading frame

(orf) analysis of the first 64 sequence tags we estimate

that up to one-third of the library is composed of genomic

DNA clones since approximately 15% of the orfs were

incorrectly oriented on the antisense strand."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 2.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTATGAGTCACC 23
|||||
Db 216 CCGTAAAGTTATTATGAGTCACC 194

RESULT 5

AA167911/c
LOCUS
DEFINITION
cPEST.003 unizAPCpIOWAsporLib1 Cryptosporidium parvum cDNA 5', similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA sequence.

ACCESSION

AA167911
VERSION
KEYWORDS
SOURCE

ORGANISM

Cryptosporidium parvum
Cryptosporidium parvum
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;

Cryptosporidiidae; Cryptosporidium.

REFERENCE

1 (bases 1 to 520)

AUTHORS

Strong, W.B. and Nelson, R.G.

TITLE

Preliminary profile of the Cryptosporidium parvum genome: an expressed sequence tag and genome survey sequence analysis

JOURNAL

Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)

PUBMED

10717299

COMMENT

Contact: Nelson, R. G.
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San Francisco
Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
Submitted sequence has been edited to remove vector sequences 5' to the insert, to correct miscalled bases and assign uncalled (N) bases throughout the sequence, and to terminate when base-calling became ambiguous.

Seq primer: M13 reverse

High quality sequence stop: 520.

Location/Qualifiers

FEATURES

source

1. 520

/organism="Cryptosporidium parvum"

/mol_type="mRNA"

/strain="IOWA"

/db_xref="taxon:5807"

/dev_stage="sporozoite"

/lab_host="E. coli XL1 Blue MRF' Kan"

/clone_lib="unizAPCpIOWAsporLib1"

/note="Vector: UniZAP XR; Site_1: EcoR I; Site_2: Xho I;

Total RNA was isolated from purified Cryptosporidium

parvum sporozoites using TRIZOL reagent (GIBCO-BRL).

Directional cDNA was synthesized by first-strand priming

with a Xho I-oligo d(T) linker-primer, second-stranding

with RNase H and DNA polymerase I, ligation of EcoR I

linkers, and digestion with Xho I, all using the

Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned

into the EcoR I and Xho I sites of Lambda Uni-ZAP XR

vector; the primary library was >97% recombinant and

contained 1.3 X 10(6) independent clones with an ca.

average insert size of 1.3 kb. Based on open reading frame

(orf) analysis of the first 64 sequence tags we estimate

that up to one-third of the library is composed of genomic

DNA clones since approximately 15% of the orfs were

incorrectly oriented on the antisense strand."

ORIGIN

Query Match 100.0%; Score 23; DB 1; Length 520;
Best Local Similarity 100.0%; Pred. No. 3;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
 |||||
 Db 238 CCGTAAAGTTATTATGAGTCACC 216

RESULT 6
 AA167858/c
 LOCUS
 DEFINITION
 similar to Cryptosporidium parvum 18S ribosomal RNA gene, mRNA

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Cryptosporidium parvum
 Cryptosporidium parvum
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Cryptosporidiidae; Cryptosporidium.
 1 (bases 1 to 566)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 COMMENT
 Contact: Nelson, R. G.
 Depts. of Medicine & Pharmaceutical Chemistry
 San Francisco General Hospital-University of California, San
 Francisco
 Box 0811, San Francisco, CA 94143-0811, USA
 Tel: 415 206 8846
 Fax: 415 206 3353

Email: malaria@itsa.ucsf.edu
 Submitted sequence has been edited to remove vector sequences 5' to
 the insert, to correct miscalled bases and assign uncalled (N)
 bases throughout the sequence, and to terminate when base-calling
 became ambiguous.
 Seq primer: M13 reverse
 High quality sequence stop: 566.

FEATURES
 source
 Location/Qualifiers
 1..566
 /organism="Cryptosporidium parvum"
 /mol_type="mRNA"
 /strain="IOWA"
 /db_xref="taxon:5807"
 /dev_stage="sporozoite"
 /lab_host="E. coli XL1 Blue MRF' Kan"
 /clone_lib="uniZAPCpIOWAsporolibi"
 /note="Vector: UniZAP XR; Site 1: EcoR I; Site 2: Xho I;
 Total RNA was isolated from purified Cryptosporidium
 parvum sporozoites using TRIzol reagent (GIBCO-BRL).
 Directional cDNA was synthesized by first-strand priming
 with a Xho I-oligo d(T) linker-primer, second-stranding
 with RNase H and DNA polymerase I, ligation of EcoR I
 linkers, and digestion with Xho I, all using the
 Stratagene ZAP-cDNA synthesis kit. The cDNA was cloned
 into the EcoR I and Xho I sites of Lambda Uni-ZAP XR
 vector; the primary library was >97% recombinant and
 contained 1.3 x 10(6) independent clones with an ca.
 average insert size of 1.3 kb. Based on open reading frame
 (orf) analysis of the first 64 sequence tags we estimate
 that up to one-third of the library is composed of genomic
 DNA clones since approximately 15% of the orfs were
 incorrectly oriented on the antisense strand."

ORIGIN
 Query Match 100.0%; Score 23; DB 1; Length 566;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
 |||||

Db 216 CCGTAAAGTTATTATGAGTCACC 194

RESULT 7
 AQ935911/c
 LOCUS
 DEFINITION

parvum rDNA gene by Blaetn analysis, genomic survey sequence.
 CpG2716B CpIOWAGDNaI Cryptosporidium parvum genomic similar to C.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 Cryptosporidium parvum
 Cryptosporidium parvum
 Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
 Cryptosporidiidae; Cryptosporidium.
 1 (bases 1 to 737)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 COMMENT
 Contact: Nelson, R. G.
 Depts. of Medicine & Pharmaceutical Chemistry
 San Francisco General Hospital-University of California, San
 Francisco
 Box 0811, San Francisco, CA 94143-0811, USA
 Tel: 415 206 8846
 Fax: 415 206 3353

Email: malaria@itsa.ucsf.edu
 For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
 Seq primer: T3
 Class: shotgun.
 Location/Qualifiers
 1..737
 /organism="Cryptosporidium parvum"
 /mol_type="genomic DNA"
 /strain="IOWA"
 /db_xref="taxon:5807"
 /la5_host="E. coli XL2 Blue MRF' "
 /clone_lib="CpIOWAGDNaI"
 /note="Vector: pBlueScript II (SK-); Site 1: EcoRV; C.
 parvum (IOWA isolate) genomic DNA was hydrodynamically
 sheared to produce fragments having a tight size
 distribution between 2-4 kb by Dr. Yvonne Thorstenson of
 the Stanford DNA Sequencing and Technology Center
 (http://sequence-www.stanford.edu/group/techdev/shear.htm)
 . The randomly sheared gDNA was chromatographed on
 Sephacryl S-400 to remove any small fragments and DNA
 eluting in the void volume was subcloned into an EcoR
 V-digested, alkaline phosphatase-treated pBlueScript II
 (SK-) vector and transformed into E. coli strain XL2 Blue
 MRF'. Recombinant clones from the first plating of the
 library were selected for sequence analysis using T3 and
 T7 primers."

ORIGIN

Query Match 100.0%; Score 23; DB 9; Length 737;
 Best Local Similarity 100.0%; Pred. No. 3.1;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
 |||||

Db 108 CCGTAAAGTTATTATGAGTCACC 86
 |||||

RESULT 8
 AJ797385/c
 LOCUS
 DEFINITION
 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
 018_40108, mRNA sequence.
 ACCESSION
 VERSION
 KEYWORDS
 EST.

AJ797385 759 bp mRNA linear EST 08-DEC-2004
 AJ797385 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
 018_40108, mRNA sequence.

AJ797385.1 GI:51112713


```

SOURCE
ORGANISM
Antirrhinum majus (snapdragon)
Antirrhinum majus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
asterids; lamiales; Plantaginaceae; Antirrhineae;
Antirrhinum.
REFERENCE
1 (bases 1 to 759)
AUTHORS
Bay, M., Stuber, K., Fellenberg, K., Schwarz-Sommer, Z., Sommer, H.,
Seidler, H. and Zachgo, S.
TITLE
Characterization of Antirrhinum Petal Development and
Identification of Target Genes of the Class B MADS Box Gene
DSFICIENS
JOURNAL
Plant Cell 16 (12), 3197-3215 (2004)
PUBMED
15539471
COMMENT
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zuechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
FEATURES
source
1..759
/organism="Antirrhinum majus"
/mol_type="mRNA"
/db_xref="taxon:4151"
/clone="018.4.01.108"
/tissue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
ORIGIN
Query Match 100.0%; Score 23; DB 1; Length 759;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CCGTAAAGTTATTATGAGTCACC 23
Db 167 CCGTAAAGTTATTATGAGTCACC 145
RESULT 9
AQ254527/c
LOCUS
DEFINITION
Cp00679B CpIOWAGDNL Cryptosporidium parvum genomic
parvum ribosomal RNA gene, genomic survey sequence.
ACCESSION
AQ254527
VERSION
AQ254527.1 GI:3725284
KEYWORDS
GSS.
SOURCE
Cryptosporidium parvum
ORGANISM
Cryptosporidiidae; Coccidia; Eimeriida;
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 770)
REFERENCE
Strong, W.B. and Nelson, R.G.
AUTHORS
Preliminary profile of the Cryptosporidium parvum genome: an
expressed sequence tag and genome survey sequence analysis
TITLE
Mol. Biochem. Parasitol. 107 (1), 1-32 (2000)
JOURNAL
10717299
PUBMED
Contact: Nelson, R. G.
COMMENT
Depts. of Medicine & Pharmaceutical Chemistry
San Francisco General Hospital-University of California, San
Francisco
Box 0811, San Francisco, CA 94143-0811, USA
Tel: 415 206 8846
Fax: 415 206 3353
Email: malaria@itsa.ucsf.edu
For Annotation Data see http://medsfgh.ucsf.edu/id/CpTags/home.html
Seq primer: T3
Class: shotgun.
Location/Qualifiers
1..770
/organism="Cryptosporidium parvum"
/mol_type="genomic DNA"
/strain="IOWA"
/db_xref="taxon:5807"
/la5_host="E. coli XL2 Blue MRF"

```

```

/clone_lib="CpIOWAGDNL1"
/notes="Vector: pBlueScript II (SK-); Site 1: EcoRV; C.
parvum (IOWA isolate) genomic DNA was hydrodynamically
sheared to produce fragments having a tight size
distribution between 2-4 kb by Dr. Yvonne Thoratenson of
the Stanford DNA Sequencing and Technology Center
(http://sequence-www.stanford.edu/group/techdev/shear.htm)
. The randomly sheared gDNA was chromatographed on
Sepharyl S-400 to remove any small fragments and DNA
eluting in the void volume was subcloned into an EcoR
V-digested, alkaline phosphatase-treated pBlueScript II
(SK-) vector and transformed into E. coli strain XL2 Blue
MRF'. Recombinant clones from the first plating of the
library were selected for sequence analysis using T3 and
T7 primers."

```

ORIGIN

```

Query Match 100.0%; Score 23; DB 9; Length 770;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy 1 CCGTAAAGTTATTATGAGTCACC 23
```

```
Db 230 CCGTAAAGTTATTATGAGTCACC 208
```

RESULT 10

```
CPA563207
LOCUS
DEFINITION
Cryptosporidium parvum GSS, PAC clone pica_0014_003, T7 end
sequence, genomic survey sequence.
ACCESSION
AJ563207
VERSION
AJ563207.1 GI:31338027
KEYWORDS
GSS; genome survey sequence.
SOURCE
Cryptosporidium parvum
ORGANISM
Cryptosporidiidae; Coccidia; Eimeriida;
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;
Cryptosporidiidae; Cryptosporidium.
1 (bases 1 to 593)
REFERENCE
Bankier, A.T., Spriggs, H.F., Partmann, B., Konfortov, B.A., Madera, M.,
Vogel, C., Teichmann, S.A., Ivens, A. and Dear, P.H.
AUTHORS
Integrated mapping, chromosomal sequencing and sequence analysis of
TITLE
Cryptosporidium parvum
JOURNAL
Genome Res. 13 (8), 1787-1799 (2003)
PUBMED
12869580
REFERENCE
2 (bases 1 to 593)
AUTHORS
Dear, P.H.
TITLE
Direct Submission
JOURNAL
Submitted (09-MAY-2003) Dear P.H., PNAC Biotech Division, MRC
Laboratory of Molecular Biology, Hills Road, Cambridge, Cambs CB2
2QH, UNITED KINGDOM
Location/Qualifiers
1..593
/organism="Cryptosporidium parvum"
/mol_type="genomic DNA"
/serotype="Type 2"
/isolate="IOWA"
/db_xref="taxon:5807"
/clone="pica_0014_003"
/dev stage="oocyst"
/notes="T7 end sequence"

```

ORIGIN

```

Query Match 91.3%; Score 21; DB 11; Length 593;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy 3 GTAAAGTTATTATGAGTCACC 23
```

```
Db 1 GTAAAGTTATTATGAGTCACC 21
```


Db 346 CCGTAAAGTTATCATGAATCACC 368

RESULT 14
DR045104/c
LOCUS

DEFINITION

DR045104 769 bp mRNA linear EST 02-JUN-2005
FP-7 G03-SEQ cDNA library of sporulating *Phaeosphaeria nodorum* SN15
on wheat cv. Amery *Triticum aestivum*/Phaeosphaeria nodorum mixed
EST library cDNA, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

DR045104 GI:66908940

EST.

Triticum aestivum/Phaeosphaeria nodorum mixed EST library

Triticum aestivum/Phaeosphaeria nodorum mixed EST library

Eukaryota; mixed EST libraries.

1 (bases 1 to 769)

Lowe, R.G.T. and Oliver, R.P.

Sporulation of *Phaeosphaeria nodorum* SN15

Unpublished (2005)

Contact: Richard Oliver

Australian Centre for Necrotrophic Fungal Pathogens (ACNFP)

Murdoch University

South Street, Murdoch, W.A 6150, Australia

Tel: +0893607404

Email: roliver@murdoch.edu.au.

Location/Qualifiers

1. 769

/organism="Triticum aestivum/Phaeosphaeria nodorum mixed

EST library"

/mol_type="mRNA"

/db_xref="taxon:331356"

/dev_stage="Sporulation"

/clone_lib="cDNA library of sporulating *Phaeosphaeria*

nodorum SN15 on wheat cv. Amery"

/note="Vector: pTriplex2; Total RNA was extracted from P.

nodorum strain SN15 infected wheat cv. Amery at 14 dpi.

Library contains both fungal and plant sequences."

FEATURES
source

ORIGIN

Query Match 86.1%; Score 19.8; DB 8; Length 769;

Best Local Similarity 91.3%; Pred. No. 1.1e+02;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTTATGATCACC 23

|||||

Db 265 CCGTAAAGTTATCATGAATCACC 243

RESULT 15
DN476855/c
LOCUS

DEFINITION

DN476855 771 bp mRNA linear EST 09-MAR-2005
altr212xell A. brassicicola mycelial culture grown under conditions
of Nitrogen Starvation *Alternaria brassicicola* cDNA clone
altr212xell, mRNA sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

DN476855 GI:60674166

EST.

Alternaria brassicicola

Alternaria brassicicola

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;

Pleosporales; Pleosporaceae; mitosporic Pleosporaceae; *Alternaria*.

1 (bases 1 to 771)

Cramer, R.A., Craven, K.D., Thon, M.R., Cho, Y., Knudson, D.L.,

Mitchell, T.K. and Lawrence, C.B.

Expressed Sequence Tag (EST) Analysis of a Compatible *Alternaria*

brassicicola-*Brassica oleracea* Interaction

Unpublished (2005)

Contact: Dr. Thomas K. Mitchell

Center for Integrated Fungal Research, NC State University

851 Main Campus Dr. Suite 233, Raleigh, NC 27606, USA

Tel: (919) 513-3926

Fax: (919) 513-0024

Email: thomas_mitchell@ncsu.edu

FEATURES
source

Seq primer: T7 SP6 primer.

Location/Qualifiers

1. 771

/organism="Alternaria brassicicola"

/mol_type="mRNA"

/strain="ATCC 96866"

/db_xref="taxon:29001"

/clone="altr212xell"

/dev_stage="mycelia"

/clone_lib="A. brassicicola mycelial culture grown under

conditions of Nitrogen Starvation"

/note="Vector: pGEMT; Mycelial culture grown under

conditions of Nitrogen Starvation."

ORIGIN

Query Match 86.1%; Score 19.8; DB 8; Length 771;

Best Local Similarity 91.3%; Pred. No. 1.1e+02;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTTATGATCACC 23

|||||

Db 238 CCGTAAAGTTATCATGAATCACC 216

.. Search completed: January 9, 2006, 21:16:57

Job time : 2476 secs

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GenCore version 5.1.6
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QM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 18:17:01 ; Search time 102.5 seconds
(without alignments)
398.867 Million cell updates/sec

Title: US-09-954-586-59

Perfect score: 23

Sequence: 1 ccgtaagattattatgagtcacc 23

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/1/ina/1 COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5 COMB.seq:*
- 3: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
- 7: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
- 8: /cgn2_6/ptodata/1/ina/6 COMB.seq:*
- 9: /cgn2_6/ptodata/1/ina/6 COMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	23	100.0	1750	3	US-08-949-770-1
C 2	18.8	81.7	439	2	US-08-093-144-3
C 3	18.8	81.7	444	2	US-08-093-144-6
C 4	18.8	81.7	446	2	US-08-093-144-4
C 5	18.8	81.7	568	3	US-09-533-559-4068
C 6	18.8	81.7	1024	3	US-09-533-559-3839
C 7	18.8	81.7	2055	3	US-10-121-740-3
C 8	18.8	81.7	2089	3	US-10-121-740-1
C 9	18.2	79.1	709	3	US-08-998-416-281
C 10	17.8	77.4	1102	3	US-10-037-417-43
C 11	17.8	77.4	1102	3	US-10-037-417-45
C 12	17.4	75.7	601	3	US-09-949-016-121653
C 13	17.4	75.7	601	3	US-09-949-016-121654
C 14	17.4	75.7	601	3	US-09-949-016-165267
C 15	17.4	75.7	601	3	US-09-949-016-165268
C 16	17.4	75.7	35263	3	US-09-949-016-12797
C 17	17.4	75.7	35263	3	US-09-949-016-16399
C 18	17.4	75.7	69737	3	US-09-949-016-15140
C 19	17.2	74.8	444	2	US-08-093-144-5
C 20	17.2	74.8	703	3	US-08-998-416-178
C 21	17.2	74.8	723	3	US-08-998-416-952
C 22	17.2	74.8	1665	3	US-09-805-127-7
C 23	17.2	74.8	1776	3	US-09-350-710B-1
C 24	17.2	74.8	1788	2	US-08-867-820A-1

C 25	16.8	73.0	92505	3	US-09-949-016-14018	Sequence 14018, A
26	16.8	73.0	130971	3	US-09-949-016-14205	Sequence 14205, A
C 27	16.6	72.2	409	3	US-09-265-585C-79	Sequence 79, Appl
C 28	16.6	72.2	1279	3	US-09-186-276B-45	Sequence 45, Appl
C 29	16.6	72.2	1279	3	US-08-842-445-45	Sequence 45, Appl
C 30	16.6	72.2	1279	3	US-09-186-188B-45	Sequence 45, Appl
C 31	16.6	72.2	1279	3	US-09-265-585C-45	Sequence 45, Appl
C 32	16.6	72.2	139562	3	US-09-949-016-13451	Sequence 13451, A
C 33	16.6	71.3	601	3	US-09-949-016-157835	Sequence 157835, A
C 34	16.4	71.3	191433	3	US-09-949-016-16144	Sequence 16144, A
C 35	16.2	70.4	601	3	US-09-949-016-141451	Sequence 141451, A
C 36	16.2	70.4	601	3	US-09-949-016-141452	Sequence 141452, A
C 37	16.2	70.4	601	3	US-09-949-016-141453	Sequence 141453, A
C 38	16.2	70.4	2059	3	US-09-489-847-119	Sequence 119, Appl
C 39	16.2	70.4	2076	3	US-09-489-847-51	Sequence 51, Appl
C 40	16.2	70.4	22846	2	US-08-469-461-3	Sequence 3, Appl
C 41	16.2	70.4	22846	3	US-07-890-609-3	Sequence 3, Appl
C 42	16.2	70.4	25122	3	US-09-949-016-16312	Sequence 16312, A
C 43	16.2	70.4	192700	3	US-09-949-016-11820	Sequence 11820, A
C 44	16.2	70.4	192704	3	US-09-949-016-17182	Sequence 17182, A
C 45	16.2	70.4	236964	3	US-09-949-016-15753	Sequence 15753, A

ALIGNMENTS

RESULT 1
US-08-949-770-1/C
; Sequence 1, Application US/08949770
; Patent No. 6063604
; GENERAL INFORMATION:
; APPLICANT: Wick, James F.
; APPLICANT: Mueller, Reinhold
; APPLICANT: Blaesak, Michele
; APPLICANT: Wilkosz, Richard K.
; TITLE OF INVENTION: Target Nucleic Acid Sequence Amplification
; Patent No. 6063604
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/949,770
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/617,045
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Pochopien, Donald J.
; REGISTRATION NUMBER: 32,167
; REFERENCE/DOCKET NUMBER: 28003/33045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312/474-6300
; TELEFAX: 312/474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1750 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; FEATURE:

; NAME/KEY: misc feature
; OTHER INFORMATION: /= "18s rRNA gene of Cryptosporidium
; OTHER INFORMATION: parvum"
US-08-949-770-1

Query Match 100.0%; Score 23; DB 3; Length 1750;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCACC 23
|||||
DB 254 CCGTAAAGTTATTATGAGTCACC 232

RESULT 2
US-08-093-144-3/c
; Sequence 3, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,192
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 439 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-093-144-3

Query Match 81.7%; Score 18.8; DB 2; Length 439;
Best Local Similarity 90.9%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGTAAAGTTATTATGAGTCACC 23
|||||
DB 156 CGAAAGTTATTATGAGTCACC 135

RESULT 3
US-08-093-144-6/c
; Sequence 6, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:

; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/745,192
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 444 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-093-144-6

Query Match 81.7%; Score 18.8; DB 2; Length 444;
Best Local Similarity 90.9%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CCGTAAAGTTATTATGAGTCACC 23
|||||
DB 156 CGAAAGTTATTATGAGTCACC 135

RESULT 4
US-08-093-144-4/c
; Sequence 4, Application US/08093144
; Patent No. 5434048
; GENERAL INFORMATION:
; APPLICANT: SIMON, LUC
; APPLICANT: LALONDE, MAURICE
; TITLE OF INVENTION: DNA PROBES FOR THE DETECTION OF
; TITLE OF INVENTION: ARBUSCULAR ENDOMYCORRHIZAL FUNGI
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
; STREET: Eleventh Floor, 1615 L. Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20036-5601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Tape
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/093,144

; FILING DATE: 435
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: US 07/745,192
; APPLICATION NUMBER: 15-AUG-1991
; FILING DATE: 15-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Hymo, Lawrence A.
; REGISTRATION NUMBER: 19,057
; REFERENCE/DOCKET NUMBER: LAH/3122/92223/MJW
; TELEPHONE: (202) 861-3000
; TELEFAX: (202) 822-0944
; TELEX: 6714627 CUSH
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 446 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-093-144-4

Query Match 81.7%; Score 18.8; DB 2; Length 446;
Best Local Similarity 90.9%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCACC 23
Db 158 CGTAAAGTTATTATGAATCACC 137

RESULT 5
US-09-533-559-4068/c
; Sequence 4068, Application US/09533559
; Patent No. 6902887
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4068
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(568)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-4068

Query Match 81.7%; Score 18.8; DB 3; Length 568;
Best Local Similarity 90.9%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCACC 23
Db 249 CGTAAAGTTATTATGATTCACC 228

RESULT 6
US-09-533-559-3839/c
; Sequence 3839, Application US/09533559
; Patent No. 6902887

; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; TITLE OF INVENTION: Expression
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/09/533,559
; CURRENT FILING DATE: 2000-03-22
; EARLIER APPLICATION NUMBER: 09/273,623
; EARLIER FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3839
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-533-559-3839

Query Match 81.7%; Score 18.8; DB 3; Length 1024;
Best Local Similarity 90.9%; Pred. No. 17;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCACC 23
Db 57 CGTAAAGTTATTATGATTCACC 36

RESULT 7
US-10-121-740-3/c
; Sequence 3, Application US/10121740
; Patent No. 6911338
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Marker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AO 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Muscodor roseus
US-10-121-740-3

Query Match 81.7%; Score 18.8; DB 3; Length 2055;
Best Local Similarity 90.9%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCACC 23
Db 245 CGTAAAGTTATTATGAATCACC 224

RESULT 8
US-10-121-740-1/c
; Sequence 1, Application US/10121740
; Patent No. 6911338
; GENERAL INFORMATION:

; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2089
; TYPE: DNA
; ORGANISM: Muscudor albus
US-10-121-740-1

Query Match 81.7%; Score 18.8; DB 3; Length 2089;
Best Local Similarity 90.9%; Pred. No. 18;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCACC 23
||| ||||| ||||| |||||
Db 258 CGTGAAGTTATTATGATCACC 237

RESULT 9
US-08-998-416-281
; Sequence 281, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgin
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGCI1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 281:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 709 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: PAG1237UP
US-08-998-416-281
Query Match 79.1%; Score 18.2; DB 3; Length 709;
Best Local Similarity 87.0%; Pred. No. 33;
Matches 20; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 CCGTAAAGTTATTATGAGTCACC 23
||| ||||| ||||| |||||
Db 418 CCGAAAAGTTATTATGATCATC 440
RESULT 10
US-10-037-417-43/c
; Sequence 43, Application US/10037417
; Patent No. 6903201
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spvtek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 1102


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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-037-417-43

Query Match      77.4%; Score 17.8; DB 3; Length 1102;
Best Local Similarity 90.5%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCA 21
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Db 92 CCGTAAAGTGAGTATGAGTCA 72

RESULT 11
US-10-037-417-45/c
; Sequence 45, Application US/10037417
; Patent No. 6903201
; GENERAL INFORMATION:
; APPLICANT: Kerkuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/10/037,417
; CURRENT FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 45
; LENGTH: 1102
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-037-417-45

Query Match      77.4%; Score 17.8; DB 3; Length 1102;
Best Local Similarity 90.5%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CCGTAAAGTTATTATGAGTCA 21
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Db 92 CCGTAAAGTGAGTATGAGTCA 72

RESULT 12
US-09-949-016-121653/c
; Sequence 121653, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121653
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-121653

Query Match      75.7%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TAAAGTTATTATGAGTCAC 22
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Db 275 TAAAGTTAGTATGAGTCAC 257

RESULT 13
US-09-949-016-121654/c
; Sequence 121654, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 121654
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-121654

Query Match      75.7%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Search completed: January 9, 2006, 21:20:29
Job time : 103.5 secs

QY 4 TAAAGTTATTATGAGTCAC 22
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Db 154 TAAAGTTAGTATGAGTCAC 136

RESULT 14

US-09-949-016-165267/c
; Sequence 165267, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165267
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-165267

Query Match 75.7%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TAAAGTTATTATGAGTCAC 22
||||||| |||||||
Db 154 TAAAGTTAGTATGAGTCAC 136

RESULT 15

US-09-949-016-165268/c
; Sequence 165268, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 165268
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-165268

Query Match 75.7%; Score 17.4; DB 3; Length 601;
Best Local Similarity 94.7%; Pred. No. 76;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 TAAAGTTATTATGAGTCAC 22
||||||| |||||||
Db 275 TAAAGTTAGTATGAGTCAC 257

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OM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 19:55:45 ; Search time 517 Seconds
(without alignments)
367.883 Million cell updates/sec

Title: US-09-954-586-59

Perfect score: 23

Sequence: 1 ccgtaaggtattatgagtcacc 23

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA Main:*

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- 2: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq.*
- 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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C 2	23	100.0	23	3	US-09-954-695-53
C 3	23	100.0	23	3	US-09-954-695-59
C 4	23	100.0	23	3	US-09-954-695-65
C 5	23	100.0	23	3	US-09-954-586-47
C 6	23	100.0	23	3	US-09-954-586-53
C 7	23	100.0	23	3	US-09-954-586-59
C 8	23	100.0	23	3	US-09-954-586-65
C 9	18.8	81.7	568	8	US-10-653-047-4068
C 10	18.8	81.7	685	6	US-10-094-097B-112
C 11	18.8	81.7	1024	8	US-10-653-047-3839
C 12	18.8	81.7	1228	9	US-10-483-433-1
C 13	18.8	81.7	2055	6	US-10-121-740-3
C 14	18.8	81.7	2055	7	US-10-623-433-3
C 15	18.8	81.7	2055	10	US-11-131-659-3
C 16	18.8	81.7	2089	6	US-10-121-740-1
C 17	18.8	81.7	2089	7	US-10-623-432-1
C 18	18.8	81.7	2089	10	US-11-131-659-1
C 19	18.4	80.0	383	6	US-10-062-674-1363
C 20	18.4	80.0	1421	8	US-10-425-115-31251
C 21	17.8	77.4	1102	7	US-10-037-417-43
C 22	17.8	77.4	1102	7	US-10-037-417-45
C 23	17.2	74.8	526	4	US-09-925-065A-384347

24	17.2	74.8	587	5	US-10-027-632-274162	Sequence 274162,
25	17.2	74.8	587	5	US-10-027-632-274162	Sequence 274163,
26	17.2	74.8	587	6	US-10-027-632-274162	Sequence 274162,
27	17.2	74.8	587	6	US-10-027-632-274162	Sequence 274163,
28	17.2	74.8	594	4	US-09-925-065A-248273	Sequence 248273,
29	17.2	74.8	594	4	US-09-925-065A-248273	Sequence 131139,
30	17.2	74.8	780	7	US-10-424-599-40289	Sequence 40289, A
31	17.2	74.8	1665	7	US-10-417-264-7	Sequence 7, Appli
32	17.2	74.8	1798	6	US-10-182-329-110	Sequence 110, App
33	17.2	74.8	1798	7	US-10-182-327-195	Sequence 195, App
34	17.2	74.8	1798	7	US-10-361-002-8	Sequence 8, Appli
35	17.2	74.8	1798	7	US-10-361-004-8	Sequence 8, Appli
36	17.2	74.8	3480	6	US-10-297-621-2	Sequence 2, Appli
37	16.8	73.0	361	6	US-10-062-674-1309	Sequence 1309, Ap
38	16.8	73.0	534	4	US-09-925-065A-610811	Sequence 610811,
39	16.8	73.0	569	4	US-09-925-065A-657517	Sequence 657517,
40	16.8	73.0	569	4	US-09-925-065A-657518	Sequence 657518,
41	16.8	73.0	596	5	US-10-027-632-223147	Sequence 223147,
42	16.8	73.0	596	6	US-10-027-632-223147	Sequence 223147,
43	16.8	73.0	598	5	US-10-027-632-216868	Sequence 216868,
44	16.8	73.0	598	5	US-10-027-632-216869	Sequence 216869,
45	16.8	73.0	598	6	US-10-027-632-216868	Sequence 216868,

ALIGNMENTS

RESULT 1

US-09-954-695-47/c
; Sequence 47, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.U7
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-47

Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTATGAGTCACC 23

Db 23 CCGTAAAGTTATTATGAGTCACC 1

RESULT 2

US-09-954-695-53/c
; Sequence 53, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.U7
; CURRENT APPLICATION NUMBER: US/09/954,695

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; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-53
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Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCGTAAAGTTATTATGAGTCACC 23
Db 23 CCGTAAAGTTATTATGAGTCACC 1
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RESULT 3

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US-09-954-695-59
; Sequence 59, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-59
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Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCGTAAAGTTATTATGAGTCACC 23
Db 1 CCGTAAAGTTATTATGAGTCACC 23
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RESULT 4

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US-09-954-695-65
; Sequence 65, Application US/09954695
; Patent No. US20020055116A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-02.UT
; CURRENT APPLICATION NUMBER: US/09/954,695
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
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; SEQ ID NO 65
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-695-65
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Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 69.6%; Pred. No. 1.2;
Matches 16; Conservative 7; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCGTAAAGTTATTATGAGTCACC 23
Db 1 CCGUAAAGUUUUUAGUCACC 23
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RESULT 5

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US-09-954-586-47/c
; Sequence 47, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-47
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Query Match 100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CCGTAAAGTTATTATGAGTCACC 23
Db 23 CCGTAAAGTTATTATGAGTCACC 1
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RESULT 6

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US-09-954-586-53/c
; Sequence 53, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic Construct
US-09-954-586-53

Query Match      100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTATGAGTCACC 23
Db 23 CCGTAAAGTTATTATGAGTCACC 1

RESULT 7
US-09-954-586-59
; Sequence 59, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-59

Query Match      100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTATGAGTCACC 23
Db 1 CCGTAAAGTTATTATGAGTCACC 23

RESULT 8
US-09-954-586-65
; Sequence 65, Application US/09954586
; Patent No. US20020146717A1
; GENERAL INFORMATION:
; APPLICANT: CUNNINGHAM, Melissa M.
; APPLICANT: STULL, Paul D.
; APPLICANT: WEISBURG, William G.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS FOR DETERMINING THE PRESENCE OF
; FILE REFERENCE: GP116-03.UT
; CURRENT APPLICATION NUMBER: US/09/954,586
; CURRENT FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/232,028
; PRIOR FILING DATE: 2000-09-12
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 23
; TYPE: RNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-09-954-586-65

Query Match      100.0%; Score 23; DB 3; Length 23;
Best Local Similarity 69.6%; Pred. No. 1.2;
```

```
Matches 16; Conservative 7; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CCGTAAAGTTATTATGAGTCACC 23
Db 1 CCGTAAAGTTATTATGAGTCACC 23

RESULT 9
US-10-653-047-4068/c
; Sequence 4068, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjørke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.200-US
; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/273,623
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4068
; LENGTH: 568
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(568)
; OTHER INFORMATION: n = A,T,C or G
US-10-653-047-4068

Query Match      81.7%; Score 18.8; DB 8; Length 568;
Best Local Similarity 90.9%; Pred. No. 1.6e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CCGTAAAGTTATTATGAGTCACC 23
Db 249 CCGTAAAGTTATTATGAGTCACC 228

RESULT 10
US-10-094-097B-112/c
; Sequence 112, Application US/10094097B
; Publication No. US20030185840A1
; GENERAL INFORMATION:
; APPLICANT: IOANNIDES, CONSTANTIN G.
; APPLICANT: PEOPLES, JR., GEORGE E.
; TITLE OF INVENTION: INDUCTION OF TUMOR IMMUNITY BY VARIANTS OF FOLATE
; FILE REFERENCE: AH-P02120US1 / UTSC:686US
; CURRENT APPLICATION NUMBER: US/10/094,097B
; CURRENT FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 10/094,097
; PRIOR FILING DATE: 2002-03-08
; PRIOR APPLICATION NUMBER: 60/274,676
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 269
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 112
; LENGTH: 685
; TYPE: DNA
; ORGANISM: Cladosporium fulvum
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (197)..(683)
```

```
; OTHER INFORMATION: N = A, C, G, or T/U
US-10-094-097B-112

Query Match      81.7%; Score 18.8; DB 6; Length 685;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      249 CGTGAAGTTATTATGATTCACC 228

RESULT 11
US-10-653-047-3839/c
; Sequence 3839, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.208-US
; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/273,623
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3839
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1024)
; OTHER INFORMATION: n = A,T,C or G
US-10-653-047-3839

Query Match      81.7%; Score 18.8; DB 8; Length 1024;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      57 CGTGAAGTTATTATGATTCACC 36

RESULT 12
US-10-483-439-1/c
; Sequence 1, Application US/10483439
; Publication No. US20050069999A1
; GENERAL INFORMATION:
; APPLICANT: Sharma, Sreenath V.
; APPLICANT: Matsushita, Noriko
; APPLICANT: Ando, Katsuhiko
; APPLICANT: Yoshida, Chitose
; APPLICANT: Nakano, Hirofumi
; APPLICANT: Agatsuma, Teutomu
; APPLICANT: Kanda, Yutaka
; TITLE OF INVENTION: SH3 DOMAIN BINDING INHIBITORS
; FILE REFERENCE: 09859/0200055-US0
; CURRENT APPLICATION NUMBER: US/10/483,439
; CURRENT FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: PCT/JP02/03932
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1

; OTHER INFORMATION: N = A, C, G, or T/U
US-10-094-097B-112

Query Match      81.7%; Score 18.8; DB 6; Length 685;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      249 CGTGAAGTTATTATGATTCACC 228

RESULT 11
US-10-653-047-3839/c
; Sequence 3839, Application US/10653047
; Publication No. US20040229367A1
; GENERAL INFORMATION:
; APPLICANT: Randy M. Berka
; APPLICANT: Michael W. Rey
; APPLICANT: Jeffrey R. Shuster
; APPLICANT: Sakari Kauppinen
; APPLICANT: Ib Groth Clausen
; APPLICANT: Peter Bjarke Olsen
; TITLE OF INVENTION: Methods For Monitoring Multiple Gene
; FILE REFERENCE: 5849.208-US
; CURRENT APPLICATION NUMBER: US/10/653,047
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/533,559
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: 09/273,623
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 7860
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3839
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Aspergillus niger
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1024)
; OTHER INFORMATION: n = A,T,C or G
US-10-653-047-3839

Query Match      81.7%; Score 18.8; DB 8; Length 1024;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      57 CGTGAAGTTATTATGATTCACC 36

RESULT 12
US-10-483-439-1/c
; Sequence 1, Application US/10483439
; Publication No. US20050069999A1
; GENERAL INFORMATION:
; APPLICANT: Sharma, Sreenath V.
; APPLICANT: Matsushita, Noriko
; APPLICANT: Ando, Katsuhiko
; APPLICANT: Yoshida, Chitose
; APPLICANT: Nakano, Hirofumi
; APPLICANT: Agatsuma, Teutomu
; APPLICANT: Kanda, Yutaka
; TITLE OF INVENTION: SH3 DOMAIN BINDING INHIBITORS
; FILE REFERENCE: 09859/0200055-US0
; CURRENT APPLICATION NUMBER: US/10/483,439
; CURRENT FILING DATE: 2004-01-09
; PRIOR APPLICATION NUMBER: PCT/JP02/03932
; PRIOR FILING DATE: 2002-04-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1

; OTHER INFORMATION: N = A, C, G, or T/U
US-10-094-097B-112

Query Match      81.7%; Score 18.8; DB 9; Length 1228;
Best Local Similarity 90.9%; Pred. No. 1.8e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      214 CGAAAAGTTATTATGAATCACC 193

RESULT 13
US-10-121-740-3/c
; Sequence 3, Application US/10121740
; Publication No. US20030186425A1
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/121,740
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Muscodor roseus
US-10-121-740-3

Query Match      81.7%; Score 18.8; DB 6; Length 2055;
Best Local Similarity 90.9%; Pred. No. 1.1e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 CGTAAAGTTATTATGAGTCACC 23
Db      245 CGTGAAGTTATTATGAATCACC 224

RESULT 14
US-10-623-432-3/c
; Sequence 3, Application US/10623432
; Publication No. US20040141955A1
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/10/623,432
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US/10/121,740
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Muscodor roseus
US-10-623-432-3
```

Query Match 81.7%; Score 18.8; DB 7; Length 2055;
Best Local Similarity 90.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCACC 23
||| ||||| ||||| |||||
Db 245 CGTGAAGTTATTATGATCACC 224

RESULT 15
US-11-131-659-3/c
; Sequence 3, Application US/11131659
; Publication No. US20050220769A1
; GENERAL INFORMATION:
; APPLICANT: Strobel, Gary
; APPLICANT: Manker, Denise
; TITLE OF INVENTION: NOVEL ENDOPHYTIC FUNGI AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: AQ 2019.40
; CURRENT APPLICATION NUMBER: US/11/131,659
; CURRENT FILING DATE: 2005-05-17
; PRIOR APPLICATION NUMBER: US/10/121,740
; PRIOR FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: 60/283,902
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/363,072
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2055
; TYPE: DNA
; ORGANISM: Muscodor roseus
US-11-131-659-3

Query Match 81.7%; Score 18.8; DB 10; Length 2055;
Best Local Similarity 90.9%; Pred. No. 1.9e+02;
Matches 20; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCACC 23
||| ||||| ||||| |||||
Db 245 CGTGAAGTTATTATGATCACC 224

Search completed: January 10, 2006, 00:04:33
Job time : 518 secs

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QM nucleic - nucleic search, using sw model

Run on: January 9, 2006, 21:17:07 ; Search time 215 Seconds
(without alignments)
77.993 Million cell updates/sec

Title: US-09-954-586-59
Perfect score: 23
Sequence: 1 ccgtaagattattatgagtcacc 23

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4637633 seqs, 364532575 residues

Total number of hits satisfying chosen parameters: 9275266

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
2: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
4: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
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6: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
7: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
9: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
10: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	17.2	74.8	1732	6	US-10-519-379-1
C 2	16.8	73.0	150437	7	US-11-112-908-44
C 3	16.8	73.0	150491	7	US-11-112-908-46
C 4	16.2	70.4	848	6	US-10-750-185-35778
C 5	16.2	70.4	848	6	US-10-750-623-35778
C 6	15.8	68.7	598	6	US-10-750-185-21192
C 7	15.8	68.7	598	6	US-10-750-623-21192
C 8	15.8	68.7	1077	6	US-10-750-185-49007
C 9	15.8	68.7	1077	6	US-10-750-623-49007
C 10	15.8	68.7	1433	6	US-10-750-185-27017
C 11	15.8	68.7	1433	6	US-10-750-623-27017
C 12	15.8	68.7	1459	6	US-10-750-185-48860
C 13	15.8	68.7	1459	6	US-10-750-623-48860
C 14	15.8	68.7	1836	6	US-10-750-185-63798
C 15	15.8	68.7	1836	6	US-10-750-623-63798
C 16	15.8	68.7	1842	6	US-10-750-185-56488
C 17	15.8	68.7	1842	6	US-10-750-623-56488
C 18	15.8	68.7	340000	7	US-11-102-978-3
C 19	15.4	67.0	1841	6	US-10-750-185-54430
C 20	15.4	67.0	1841	6	US-10-750-623-54430
C 21	15.2	66.1	25	7	US-11-121-849-664285
C 22	15.2	66.1	201	6	US-10-995-561-78246
C 23	15.2	66.1	853	6	US-10-750-185-54024

ALIGNMENTS

RESULT 1
US-10-519-379-1/c
; Sequence 1, Application US/10519379
; Publication No. US20050255126A1
; GENERAL INFORMATION:
; APPLICANT: ASAHI DENKA Co., Ltd.
; TITLE OF INVENTION: New microorganism and method for producing aglucan by the new
; TITLE OF INVENTION: microorganism
; FILE REFERENCE: A0301
; CURRENT APPLICATION NUMBER: US/10/519,379
; CURRENT FILING DATE: 2004-12-27
; NUMBER OF SEQ ID NOS: 4
; SEQ ID NO 1
; LENGTH: 1732
; TYPE: DNA
; ORGANISM: Aureobasidium pullulans ADK-34
US-10-519-379-1

Query Match 74.8% Score 17.2; DB 6; Length 1732;
Best Local Similarity 86.4%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCACC 23
Db 223 CGTTAGTTATTATGATCACC 202

RESULT 2
US-11-112-908-44
; Sequence 44, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; TITLE OF INVENTION: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; CURRENT FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07

Sequence 54024, A
Sequence 43, Appl
Sequence 44132, A
Sequence 44132, A
Sequence 26452, A
Sequence 26452, A
Sequence 2, Appl
Sequence 45040, A
Sequence 45040, A
Sequence 1, Appl
Sequence 2929, Ap
Sequence 13475, A
Sequence 393, App
Sequence 2900, Ap
Sequence 69, Appl
Sequence 58799, A
Sequence 492, App
Sequence 493, App
Sequence 494, App
Sequence 29436, A
Sequence 29436, A
Sequence 13340, A

; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 44
; LENGTH: 150437
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-44

Query Match 73.0%; Score 16.8; DB 7; Length 150437;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCA 21
| | | | | | | | | | | | | | | | | |
Db 122551 CATAAAGTTATTATGAGTTA 122570

RESULT 3
US-11-112-908-46
; Sequence 46, Application US/11112908
; Publication No. US20050260659A1
; GENERAL INFORMATION:
; APPLICANT: Harris, Cole
; APPLICANT: Davis, Lisa M.
; TITLE OF INVENTION: Breast Cancer Biomarkers
; FILE REFERENCE: 04-164-US
; CURRENT APPLICATION NUMBER: US/11/112,908
; PRIOR FILING DATE: 2005-04-22
; PRIOR APPLICATION NUMBER: US 60/564,758
; PRIOR FILING DATE: 2004-04-23
; PRIOR APPLICATION NUMBER: US 60/575,978
; PRIOR FILING DATE: 2004-06-01
; PRIOR APPLICATION NUMBER: US 60/631,702
; PRIOR FILING DATE: 2004-11-30
; PRIOR APPLICATION NUMBER: US 60/633,826
; PRIOR FILING DATE: 2004-12-07
; NUMBER OF SEQ ID NOS: 511
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 46
; LENGTH: 150491
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-112-908-46

Query Match 73.0%; Score 16.8; DB 7; Length 150491;
Best Local Similarity 90.0%; Pred. No. 1.2e+02;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCA 21
| | | | | | | | | | | | | | | | | |
Db 59077 CATAAAGTTATTATGAGTTA 59096

RESULT 4
US-10-750-185-35778
; Sequence 35778, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 35778
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Bovine 19866881182167
US-10-750-185-35778

Query Match 70.4%; Score 16.2; DB 6; Length 848;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCAC 22
| | | | | | | | | | | | | | | | | |
Db 8 CGTAAATTTATTATGAACCCAC 28

RESULT 5
US-10-750-623-35778
; Sequence 35778, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35778
; LENGTH: 848
; TYPE: DNA
; ORGANISM: Bovine 19866881182167
US-10-750-623-35778

Query Match 70.4%; Score 16.2; DB 6; Length 848;
Best Local Similarity 85.7%; Pred. No. 1.6e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 CGTAAAGTTATTATGAGTCAC 22
| | | | | | | | | | | | | | | | | |
Db 8 CGTAAATTTATTATGAACCCAC 28

RESULT 6
US-10-750-185-21192/c
; Sequence 21192, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21192
; LENGTH: 598
; TYPE: DNA

; ORGANISM: Bovine MMBT01950
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(64)
; OTHER INFORMATION: n is any nucleotide
US-10-750-185-21192

Query Match 68.7%; Score 15.8; DB 6; Length 598;
Best Local Similarity 81.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCAC 22
:|||||
Db 531 YGTAAAGTTATTATTGTGAC 511

RESULT 7
US-10-750-623-21192/c
; Sequence 21192, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 21192
; LENGTH: 598
; TYPE: DNA
; ORGANISM: Bovine MMBT01950
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(64)
; OTHER INFORMATION: n is any nucleotide
US-10-750-623-21192

Query Match 68.7%; Score 15.8; DB 6; Length 598;
Best Local Similarity 81.0%; Pred. No. 2.4e+02;
Matches 17; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 CGTAAAGTTATTATGAGTCAC 22
:|||||
Db 531 YGTAAAGTTATTATTGTGAC 511

RESULT 8
US-10-750-185-49007/c
; Sequence 49007, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31

; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 49007
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Bovine 19866880353038
US-10-750-185-49007

Query Match 68.7%; Score 15.8; DB 6; Length 1077;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTAAAGTTATTATGAGTCA 21
:|||||
Db 892 GTAAAGTTATTATAGTCA 874

RESULT 9
US-10-750-623-49007/c
; Sequence 49007, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 49007
; LENGTH: 1077
; TYPE: DNA
; ORGANISM: Bovine 19866880353038
US-10-750-623-49007

Query Match 68.7%; Score 15.8; DB 6; Length 1077;
Best Local Similarity 89.5%; Pred. No. 2.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GTAAAGTTATTATGAGTCA 21
:|||||
Db 892 GTAAAGTTATTATAGTCA 874

RESULT 10
US-10-750-185-27017
; Sequence 27017, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 27017

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; LENGTH: 1433
; TYPE: DNA
; ORGANISM: Bovine 19866881858622
US-10-750-185-27017

Query Match      68.7%; Score 15.8; DB 6; Length 1433;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAAGTTATTATGAGTCACC 23
Db 523 AAAGATATTATGACTCACC 541

RESULT 11
US-10-750-623-27017
; Sequence 27017, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 27017
; TYPE: DNA
; ORGANISM: Bovine 19866881858622
US-10-750-623-27017

Query Match      68.7%; Score 15.8; DB 6; Length 1433;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAAGTTATTATGAGTCACC 23
Db 523 AAAGATATTATGACTCACC 541

RESULT 12
US-10-750-185-48860
; Sequence 48860, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 48860
; TYPE: DNA
; ORGANISM: Bovine 19866880620497

US-10-750-185-48860

Query Match      68.7%; Score 15.8; DB 6; Length 1459;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAAGTTATTATGAGTCACC 23
Db 709 AAAGTTATTATGAGTTACC 727

RESULT 13
US-10-750-623-48860
; Sequence 48860, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 48860
; LENGTH: 1459
; TYPE: DNA
; ORGANISM: Bovine 19866880620497
US-10-750-623-48860

Query Match      68.7%; Score 15.8; DB 6; Length 1459;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 AAAGTTATTATGAGTCACC 23
Db 709 AAAGTTATTATGAGTTACC 727

RESULT 14
US-10-750-185-63798/c
; Sequence 63798, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 63798
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Bovine 19866880348213
US-10-750-185-63798

Query Match      68.7%; Score 15.8; DB 6; Length 1836;
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Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TAAAGTTATTATGAGTCAC 22
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Db 1221 TAAAAATTATTGACTCAC 1203

RESULT 15
US-10-750-623-63798/c
; Sequence 63798, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63798
; LENGTH: 1836
; TYPE: DNA
; ORGANISM: Bovine 19866880348213
US-10-750-623-63798

Query Match 68.7%; Score 15.8; DB 6; Length 1836;
Best Local Similarity 89.5%; Pred. No. 2.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 TAAAGTTATTATGAGTCAC 22
 |||||
Db 1221 TAAAAATTATTGACTCAC 1203

Search completed: January 10, 2006, 00:11:54
Job time : 217 secs

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